14, Appl 14, Appl 76, Appl 76, Appl 76, Appl 3, Appli 3, Appli 3, Appli 7, Appli 7, Appli 7, Appli

Sequence Sequence

Sequence 3, P Sequence 3, P Sequence 3, P Sequence 7, P

Sequence 7, Sequence 2, Sequence 2,

Seguence

Sequence 14, 1 Sequence 2, Al Sequence 76, Sequence 76,

Sequence Sequence Sequence

OM protein

Run on:

Sednence:

Title:

Searched:

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100.0%; Score 53; DB 1; Length 9; 100.0%; Pred. No. 2e+05; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Dimitrios T. Drivas, White and Case STREET: 1155 Avenue of the Americas CITY: New York COUNTRY: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
US-08-488-351A-99
US-08-488-151A-95
US-08-488-313A-95
US-09-079-372-14
US-09-174-263-2
US-08-446-692-76
US-08-488-31A-76
US-08-488-31A-76
US-08-480-370-3
US-08-447-21A-3
US-08-480-370-3
US-08-446-478A-7
US-08-474-988B-7
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US-08-474-988B-2
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                                                                                                                                                                        US-08-394-442B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,219
FILING DATE: 12-NOV-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Drivas, Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-028
TELECOMMUNICATION:
                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 819-8286
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
  FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
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   RESULT 1
   Sequence 100, App
Sequence 100, App
Sequence 99, Appl
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Sequence 4, Appli
Sequence 1, Appli
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Sequence 9, Appli
Sequence 16, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                     5, 2003, 09:46:51; Search time 9.85714 Seconds (without alignments) 26.864 Million cell updates/sec
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Sequence 100,
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Sequence 4,
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-622-971-10

US-08-991-935A-10

US-08-91-935A-10

US-08-151-219-4

PCT-US94-13205-4

PCT-US94-13205-1

US-08-131-219-1

US-08-13205-1

US-08-146-692-75

US-08-446-692-75

US-08-446-692-75

US-09-079-372-17

US-09-079-372-17

US-09-079-372-15

US-09-079-372-15

US-09-079-372-15

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US-08-446-692-99
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US-08-446-692-100
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-08-488-351A-69
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                              protein search, using
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Maximum DB seq length: 200000000
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53
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Query
Match Length D
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ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 53; DB 2; Length 12; 100.0%; Pred. No. 0.0043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                             ZIP: 94080

COMPUTER READABLE FORM.

COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PattentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLING DATE: 17-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
: 460 Point San Bruno Blvd.
South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,971
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/08991258A Patent No. 5928887
                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P103
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 225-3216
TELEFAX: (415) 922-9881
TELEX: 910 371-7168
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Dreger, Walter H. REGISTRATION NUMBER: 24,190
                                                            United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 17-DEC
CLASSIFICATION: 435
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                                                            COUNTRY: U
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0
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APPLICANT: Grams, Stephen
APPLICANT: Michaell, Dov
APPLICANT: Michaell, Dov
APPLICANT: Michaell, Dov
APPLICANT: Michaell, Dov
TITLE OF INVENTION: IMPROVED IMMUNOCENIC COMPOSITIONS
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dimitrios T. Drivas, White and Case
STRRET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08652971
Patent No. 5814507
GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5; Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13205
FILING DATE: 12 NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Drivas, Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-028
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 53, 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New York
COUNTRY: U.S.A.
2IP: 100036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                         Sequence 2, Application PC/TUS9413205 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (212),819-8286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 354 8113
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
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GY: linear
            ECPWLEEEE 9
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EGPWLEEEE 9
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                                                                                                                                   PCT-US94-13205-2
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 53; DB 2; Length 12; Pred. No. 0.0043; Mismatches 0; Indels
                                                                                                                                                                                                                                              Length 12;
                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTMARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,399
                                                                                                                                                                                                                                        100.0%; Score 53; DB 2; 100.0%; Pred. No. 0.0043;
                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd.
CITY: South San Francisco
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08769399
Patent No. 5976852
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: P1 TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cheng, Jill APPLICANT: Lasky, Laurence A.
                                                                           INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 225-3216
TELEFAX: (415) 952-9881
TELEX: 910 371-716
INFORMATION FOR SEQ ID NO: 10
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                   TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 amino acids
                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
'TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                      ; TOPOLOGY: linear
; MOLEGULE TYPE: protein
US-08-991-258A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-769-399-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Best Local Similarity
Matches 9; Conserv
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EGPWLEEEE
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                                                                                                                                                                                                                         ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP STREET: 4 Embarcadero Center, Suite 3400
STRETT: San Francisco
STATE: California
COUNTRY: United States
                                                                                 APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 53; DB 3; Length 12; 100.0%; Pred. No. 0.0043; ive 0; Mismatches 0; Indels
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; Patent No. 5468494
; GENERAL INFORMATION:
APPLICANT: Gevas, Philip C.
APPLICANT: Arr, Stephen
APPLICANT: Michaell, Dov
APPLICANT: Scibienski, Robert
TITLE OF INVENTION: IMPROVED IMMUNOSENIC COMPOSITIONS
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,953A FILING DATE: 16-DEC-1997 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Dimitrios T. Drivas, White and Case 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A-63478-3/WHD/MTK
                Sequence 10, Application US/08991953A Patent No. 6083748
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Dreger, Walter H. REGISTRATION NUMBER: 24,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                         ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 11
US-08-991-953A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-991-953A-10
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US-08-151-219-4
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     ; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
PCT-US94-13205-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ), ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-151-219-1
                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100...
                                                                 15 amino acids
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                    amino acid
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TRY: U.S.A.
100036
                                                                                                                                                                                                                                                                                                                                      1 EGPWLEEEE 9
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                                                                                                    TOPOLOGY:
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US-08-151-219-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Geras, Philip C.
APPLICANT: Geras, Stephen
APPLICANT: Grimes, Stephen
APPLICANT: Machaeli, Dov
APPLICANT: Michaeli, Dov
APPLICANT: Michaeli, Dov
APPLICANT: Scibienski Robett
TITLE OF INVENTION: IMPROVED IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
NUMBER OF INVENTION: AGAINST HUMAN GASTRIN 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dimittrios T. Drivas, White and Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
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                   COUNTRY: U.S.A.

ZIP: 100036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Data Floppy disk
FLING DATE: Data Floppy disk
CLASSIFICATION NUMBER: US/08/151,219
FLING DATE: 12-NOV-1993
CLASSIFICATION: Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-028
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 4:
FLEERAL (212) 354-8113
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
2IP: 100036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US94/13205
FILING DATE: 12-NOV-1993
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NAME: Drivas, Dimitrios T.
REGISTRATION NUMBER: 32,218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 9; Conserv
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INFORMATION FOR SEQ 1D NO: 4:

SEQUENCE CHARACTRESTICS:

INCLEMENT: 13 anino acids

TAPE: anino acids

TAPE:
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us-09-700-329-1.rai

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TELEPHONE:
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US-08-446-692-75
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                                                                                                                FEATURE:
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Patent No. 6335176
GENERAL INFORMATION:
APPLICANT: Inglese, James
APPLICANT: Glickman, Joseph Fraser
TITLE OF INVENTION: Incorporation of Phosphorylation Sites
FILE REFERENCE: 1073.050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                        APPLICANT: Grams, Philip C.
APPLICANT: Grimes, Stephen
APPLICANT: Marr, Stephen
APPLICANT: Michaeli, Dow
APPLICANT: Michaeli, Dow
APPLICANT: Michaeli, Dow
TITLE OF INVENTION: IMPROVED IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dimitrios T. Drivas, White and Case STREET: 1155 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 53; DB 5; 100.0%; Pred. No. 0.0059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Drivas, Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-028
TELECOMMUNICATION INFORMATION:
TELEPAN: (212) 819-8286
TELEPAN: (212) 354-8113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/174,216A CURRENT FILING DATE: 1998-10-16 NUMBER OF SEQ ID NOS: 8 SOFTWARE: PATENTIN VEr. 2.1 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13205
FILING DATE: 12-NOV-1993
                                                                                                            Sequence 1, Application PC/TUS9413205
GENERAL INFORMATION:
APPLICANT: Gevas, Philip C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
COUNTRY: U.S.A. |
ZIP: 100036 |
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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1 EGPWLEEEE 9
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                                                                          RESULT 10
PCT-US94-13205-1
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TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
UNUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Designed OTHER INFORMATION: peptide to act as kinase substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 53; DB 4; Length 17; 100.0%; Pred. No. 0.0062; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.3%; Score 50; DB 1; Length 12; 88.9%; Pred. No. 0.014; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
COOMPRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAECENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/446,692
APPLICATION NUMBER: US/08/446,692
                                                                                                                                                                                                                                                                          NAME/KEY: MOD_RES
LOCATION: (1)
COTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-09-174-216-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 75, Application US/08446692; Patent No. 5759551; GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Maria C.H. Lin
345 Park Avenue
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (212)415-8745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (516)751-6849 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 amino acids
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Best Local Similarity الاست.
الا كانت المتحدد وي المتحدد ويتحدد المتحدد ا
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EGPWLEEEE 9
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CORRESPONDENCE ADDRESS:
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US-08-488-351A-75

Sequence 75, Application US/08488351A

Patent No. 584346

GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
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                                                                                                                                                                                                                                                                                     ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STREET: NY
COUNTRY: US
ZTREE: NY
COUNTRY: US
ZTREE: NY
COUNTRY: US
ZTREE: NY
CONPUTER: ELOPPY disk
COMPUTER: ELOPPY disk
COMPUTER: ELOPPY disk
COMPUTER: ELOPPY disk
COMPUTER: PARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible;
COMPUTER: PARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible;
COMPUTER: TBM PC Compatible;
COMPUTER: TAND NOWER: US/08/488,351A
FILING DATE: 7-UNN-1995
CLASSIFICATION NUMBER: US 08/29,275
FILING DATE: 14-APR-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING APPLICATION NUMBER: US 08/057,166
FILING APPLICATION NUMBER: US 08/057,166
FILING APPLICATION NUMBER: 1932
REFERENCE/CONCKET NUMBER: 1151-4146 US2
TELECOMMUTCATION INFORMATION:
MAME: MATA C.H. LIN
REGISTRATION NUMBER: 1151-4146 US2
TELECOMMUTCATION INFORMATION:
MORE: MATA C.H. LIN
REFERENCE/CONCKET NUMBER: 1151-4146 US2
TELECOMMUTCATION INFORMATION:
MORE: MATA C.H. LIN
REFERENCE/CONCKET NUMBER: 1151-4146 US2
TELECOMMUTCATION INFORMATION:
MORE: MORE: MATA C.H. LIN
REFERENCE/CONCKET NUMBER: 1151-4146 US2
TELECOMMUTCATION INFORMATION:
MORE: MORE: MORE: 1151-4146 US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. v.v.
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Pred. No. (
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Patent No. 5759551
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (516)751-649
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.9
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MOLECULE TYPE: peptide
US-08-488-351A-75
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US-08-446-692-74
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US-08-488-351A-74

Sequence 74, Application US/08488351A

PAPLICANT: Ladd, Anna

APPLICANT: Wang, Chang Yi

APPLICANT: Wang, Chang Yi

APPLICANT: Wang, Chang Yi

APPLICANT: Wang, Chang Yi

APPLICANT: APPLICANT: Immunogenic LHRH peptide constructs

TITLE OF INVENTION: Immunogenic LHRH peptide constructs

TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSED: Maria C.H. Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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0
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Pred. No. 0.02;
1; Mismatches 0; Indels
                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: 10154-0053
COUNTRY: US
ZIP: 10154-0053
COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-40N-1995
CLASSEFICATION - 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 7-10W-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-10W-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 08/229,275
                                                                                                                                                                                                                                                                                                                                                                CLASSLELALALM, 12.
ATTORNEY/AGENT INFORMATION:
NAME: MATIA C. H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/CDOCKET NUMBER: 1151-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEPHONE: (212)415-8745
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 anino acids
  Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.3%;
88.9%;
ADDRESSEE: Maria C.H. Li
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-08-446-692-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                               New York
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0
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94.3%; Score 50; DB 2; Length 17;

Best Local Similarity 88.9%; Pred. No. 0.02;

Matches 8; Conservative 1; Mismatches 0; Indels
FILING DATE: 14-AFR-1994
CLASSIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-AFR-1992
CLASSIPICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 1151-4146 US2
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8445
TELEFANCE (145751-6849
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: peptide
US-08-488-351A-74
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February 5, 2003, 09:40:45; Search time 26.5714 Seconds (without alignments) , 45.133 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                     908470
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                           908470 segs, 133250620 residues
                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                              US-09-700-329-1
53
1 EGPWLEEEE 9
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                                                                                                                                                                                                                      Perfect score:
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                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                       Run on:
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Database :

| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
| SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1984.DAT:*
| SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1985.DAT:*
| SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1986.DAT:*
| SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1988.DAT:*
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| SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1989.DAT:*
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| SIDS2/gcgdata/geneseqg/geneseqg-embl/AA1980.DAT:*
| SIDS2/gcgdata/geneseqg/geneseqg-embl/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			Description	Anti-qastrin-17 im	Human qastrin amin	Antidastrin-G17 im	Antigenic peptide	Human gastrin 17 a	Human gastrin 17 a	Human heptadecadas	Gastrin fragment a	Carboxy-amidated q	Human Janus kinase	
COTTAGATOO			QI	AAW24399	AAY51305	AAY59434	AAR06245	AAR74297	AAR74295	AAY49309	AAW65184	AAW24398	AAU05580	
				18	21	21	11	16	16	21	17	18	22	
			Match Length DB	6	6	6	12	15	16	16	17	17	17	
	фP	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
			Score	53	53	53	53	53	53	53	53	53	53	
		Result	No.	Н	7	m	4	2	9	7	89	O	10	

Grimes S, Karr SL, Michaeli D, Watson SA;

PC,

Gevas

Gastrin releasing KS2-peptide substr Protein kinase A (Glycine-extended g Gastrin hapten. H	amidated ga glygastrin progastrin in processin progastrin progastrin ted gastrin	releasing ogastrin idated ga gastrin ogastrin nic gastr nic gastr		psis trans ic peptide psis thali ITHP polyp ovel secre
AAB9124 AAB5927 AAU7650 AAW2439 AAR6274	AAY72 AAY72 AAY72 AAY72 AAW31 AAW31	AAB9124 AAY7238 AAY7238 AAW3163 AAY7237 AAK6275 AAR6274 AAR6274	AAY7237 AAY7238 AAP9033 AAU7440 AAP71246 AAB1376	AAU9306 AAR0624 AAY0583 ABG6000 AAU1625
000444	121221211	334 223 34 222 334 222 335 183 52 185 152 153 153 153	108010001	
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00 00 00 00 00	800 800 800 800	00000000000000000000000000000000000000) N N N N A 4 4 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 4 4 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0
11 12 13 14 15	17 18 20 21 22 23 24	255 265 27 23 33 33 33 33	33 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 3 2 4 4 5 4 4 3

ALIGNMENTS

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/note= "Glu modified by a peptide spacer conjugated to
    a diphtheria toxoid"
                                                                                          Glycine-extended gastrin-17; gastrointestinal tumour; immunogen; colorectal adenocarcinoma; antibody; progastrin; cholecystochinin B; anti-gastrin-17; anti-G-17.
                                                                                                                                            Location/Qualifiers
9
                  AAW24399 standard; peptide; 9 AA.
                                                                                                                                                                                                                                   97WO-US02029.
                                                                                                                                                                                                                                                      96US-0011411.
                                                       (first entry)
                                                                         Anti-gastrin-17 immunogen.
                                                                                                                                                                                                                                                                        (APHI-) APHION CORP.
                                                                                                                                                  Key
Modified-site
                                                                                                                                                                                              W09728821-A1.
                                                                                                                                                                                                                                  07-FEB-1997;
                                                                                                                                                                                                                                                      08-FEB-1996;
                                                                                                                                Homo sapiens
                                                                                                                                                                                                                  14-AUG-1997.
                                                     13-MAR-1998
                                    AAW24399;
RESULT 1
         AAW24399
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<del>, |</del>
                                                                                                                                                                                                                         AAY59434
                                                                                                                                                                                                             RESULT
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                                                                                                   The present sequence represents a specific example of an anti-gastrin-17 inmunogen, comprising the N-terminal 9 amino acids of gastrin-17 conjugated to an immunogenic carrier such as Diphtheria toxoid, by a spacer peptide. This immunogenic composition is used in a new treatment of glycine-extended gastrin-17 (G17-G1y)-dependent gastrointestinal tumnours. Anti-G17 immunogenic composition is used in a new treatment tumnours. Anti-G17 immunogens raise antibodies which bind both the amidated and glycine-extended forms of G17. Neutralisation of progastrin G17-G1y prohormone by the antibodies inhibits the growth of tumour cells dependent on progastrin G17-G1y as growth stimulator or inducer. The method is especially for the treatment of colorectal adenocarcinomas in humans. The novel method is non-invasive, selectively reversible, does not damage normal tissue, does not require frequent repeated treatments and does not cross the blood brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic; treatment; hypergastrinemia; gastrin G17; gastrin G34; /
pernicious anemia; anti-ulcer; proton pump inhibitor; colorectal diséase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel method for the treatment or preventing hypergastrinemia by administering the a patient a gastrin G17 and/or G34 peptide fragment linked by an amino acid spacer to an immunogenic carrier. The methods are used to treat hypergastrinemic patients, particularly those with pernicious anemia, those receiving treatment with anti-ulcer agents such as proton pump inhibitors (particularly
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating or preventing hypergastrinemia comprising administration of, e.g. anti-gastrin antibodies -
                         Treatment of glycine-extended gastrin-17-dependent gastrointestinal tumours - using anti-617 immunogenic composition, especially for
                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                               Length 9;
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watson
                                                                                                                                                                                                                                                                                                            Score 53; DB 18;
Pred. No. 7.8e+05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gastrin aminoterminal (1-9) G17 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Michaeli D,
                                                   treatment of colorectal adenocarcinomas
                                                                            Example 1; Figure 1C; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 11; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY51305 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                               100.0%;
100.0%;
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Best Local Similarity 100.
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WPI; 1997-415075/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-116301/10.
                                                                                                                                                                                                                                                                                      9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                 1 EGPWLEEEE
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                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY51305
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                                                                                                                                                                                                                       Gaps
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                                                S
omeprazole or lansoprazole) or H_2 receptor blocking agents or antagonists, or those having colorectal disorders or diseases. T sequence represents the human gastrin G17 peptide which is used illustrate the method of the invention.
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                                                                                                                                                                      Length 9;
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                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumour; tumour growth factor;
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                                                                                                                                                                      100.0%; Score 53; DB 21; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "pyroglutamic acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY59434 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US10750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      over chemotherapy alone.
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                                                                                                                                                                                         Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                   EGPWLEEEE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 AA;
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                                                                                                                          AA;
                                                                                                                                                                                                                                                                                              EGPWLEEEE
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                                                                                                                                                                        Query Match
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Scibienski

Michaeli D,

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Grimes S,
    (APHT-) APHTON CORP
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                                                                                                                                                                                                                                                                                                                                              Synthetic
                    Gevas PC,
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                                                                                                                                                                                                                                                                   AAR74295;
                                                                                                                                                 Sequence
                                                                                                                                                                                                                                     RESULT 6
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                                                                                                                                                                                                                             Immunogens against gastrin peptide(s) - used to induce antibodies that specifically neutralise single form of gastrin, G17 or \rm G34
                                                                   of
                                                                                         Gastrin; tumours; peptic ulcers; diptheria toxoid; tetanus toxin;
                                                                 Antigenic peptide fragment selected from the 12 N-terminal AAs heptadecagastrin (G17).
                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                   Antigenic fragments may be attached to an immunogenic carrier and used to raise Abs to a specific single form of Gastrin ie. G17 or G34. Peptide fragments capable of binding to these Abs are useful in neutralising anti-gastrin Abs in vivo.
                                                                                                                                                                                                                                                                                                                       100.0%; Score 53; DB 11; Length 12; 100.0%; Pred. No. 0.023; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gastrin 17 antigenic peptide hG17(1-9)-Arg9.
                                                                                                                                                                                               Littenberg RL;
                                                                                                                                                                                                                                                                                                                                                                                                             AAR74297 standard; peptide; 15, AA.
                   12 AA:
                                                                                                                                                                                                                                                     Claim 6; Page 19; 32pp; English.
                                                                                                                                                                                                Karr SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94WO-US13205.
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                                                                                                                                        90EP-0300456.
                                                                                                                                                        89US-0351193
89US-0301353
                       AAR06245 standard; peptide;
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                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                Grimes S,
                                                                                                                                                                                 (APHT-) APHTON CORP.
                                                                                                                                                                                                              WPI; 1990-233029/31
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                         12 AA;
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24-JAN-1989;
                                                     07-DEC-1990
                                                                                                                          01-AUG-1990
                                                                                                           EP380230-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                               Gevas PC,
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                                                                                                                                                                                                                                                                                                           Seguence
                                      AAR06245;
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
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                 AAR06245
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                                                                                                                                                                                                                                                       AAR74295 and AAR74297 are human gastrin 17 (hG17) antigenic peptides, used to produce anti-hG17 antibodies (Abs). The Abs can be induced in a patient, or used for passive immunisation, for the treatment of diseases in which hG17 is involved, e.g. gastric and duodenal ulceration; gastro-oesophageal reflux disease and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                          Immunogenic compsn. for producing anti-human gastrin 17 antibodies - used for treating e.g. gastro-oesophageal reflux disease, gastric and duodenal ulceration or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gastrin 17; antigenic peptide hG17(1-9)-Ser9; immunisation; treatment; gastro-oesophageal reflux disease; gastric; duodenal; ulceration; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 53; DB 16; Length 15; 100.0%; Pred. No. 0.029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR74295 standard; peptide; 16 AA.
                                                                                                                                                                                                              Example 1; Page 3; 17pp; English.
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Karr SL,
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Best Local Similarity
7, Conserve
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                                                 WPI; 1995-194034/25
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1 EGPWLEEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the treatment of gastroesophageal reflux disease (GERD) that comprises administering to a patient an immunogenic composition which generates anti-gastrin antibodies, which bind to gastrin, in a patient, and administering histamine H_2 antagonist or a proton pump inhibitor: The method provides a more effective method for controlling acid output by the stomach. The therapy is less costly. High gastrin levels associated with standard therapies are neutralized and undestrable side effects are reduced. The method permits a reduced dosage of acid reducing agent both at the acid production of dosages is acid production stimulating level (gastrin). Reduction of dosages is acid production stimulating level (gastrin). Reduction of dosages is acid production prologed treatment of GERD. In a combination therapy with H_2 agonists or proton pump inhibitors, anti-gastrin 17 antibody titers can be maintained by occasional bodster shots while gastric acid the esophagists to completely heal and no surgery is required. The present sequence represents a human heptadecagastrin (GI7) immunomimic
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                                                                                                                                                                                                                                                                                                                                                     Gastroesophageal reflux disease; GERD; gastrin; anti-gastrin antibody; histamine H_2; proton pump inhibitor; acid output; stomach; therapy; esophagitis; immunogen; human; heptadecagastrin; immunomimic; G17.
                                                                                                                                                                                                                                                                                                                     Human heptadecagastrin (G17) immunomimic with carboxy terminal spacer.
                                                       Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method for treatment of gastroesophageal reflux disease (GERD)
                      Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 53; DB 21; Length 16;
                                                      0; Indels
                    Score 53; DB 16;
Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "carboxy-terminal spacer"
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Michaeli D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= pglu
/note= "pyroglutamate"
10..16
/note= "carboxy-termin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      followed by a carboxy-terminal spacer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Page 13; 24pp; English.
                                                                                                                                                                                                                AAY49309 standard; peptide; 16 AA.
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0
                100.0%;
ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
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                                                                                                                                                                                                                                                                                     (first entry)
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Query Match
Best Local Similarity
'. ~ 9; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-062378/05
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                                                                                                              1 EGPWLEEEE 9
                                                                                       1 EGPWLEEEE
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Bradykinin; N-benzylglycine; agonist; receptor study; antagonist; achiral; analgesic; angiotensin II; gastrin.
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bradykinin agonists or antagonists, useful e.g. as analgesics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 53; DB 17; Length 17; Best Local Similarity 100.0%; Pred. No. 0.033; Matches 9; Conservative 0; Mismatches 0; Indels
No. 0.031;
                 Pred. No. 0.(
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Pyroglutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                       AAW65184 standard; peptide; 17 AA.
  100.08; Pit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89US-0376839.
92US-0945664.
94US-0335202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0335202
                                                                                                                                                                                                                                                                                                                                                  Gastrin fragment analogue.
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
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                 Best Local Similarity
Matches 9; Conserv
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EGPWLEEEE 9
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EGPWLEEEE
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-1994;
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07-NOV-1994;
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                                                                                                                                                                                                                                                                                                        02-0CT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                              AAW65184;
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ID AAW2
XX
AC AAW2
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Synthetic.

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The present sequence represents carboxy-amidated gastrin-17. Treatment of gastrin-17-dependent gastrointestinal tumours comprises administering to a mammal an anti-gastrin 17 (G17) immunogenic composition. Anti-G17 immunogens raise antibodies which bind both the amidated and glycine-extended forms of G17. Neutralisation of progastrin G17-G1y prohormone by the antibodies inhibits the growth of tumour cells dependent on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 progastrin G17-G1y as growth stimulator or inducer. The method is especially for the treatment of colorectal adenocarcinomas in humans. This novel method is non-invasive, selectively reversible, does not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                         carboxy-amidated gastrin-17; gastrointestinal tumour; immunogen;
colorectal adenocarcinoma; antibody; progastrin; cholecystochinin B.
anti-gastrin-17; anti-G-17.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Treatment of glycine-extended gastrin-17-dependent gastrointestinal tumours - using anti-G17 immunogenic composition, especially for treatment of colorectal adenocarcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             damage normal tissue, does not require frequent repeated treatments and does not cross the blood brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Janus kinase 3; JAK/STAT inhibitor; peptide substrate; signal transducer and activator of transcription; osteoarthritis; degenerative joint disease; rheumatoid arthritis; leprosy; asthma; cancer; tumour; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Janus kinase 3 (JAK3) biotinylated peptide substrate GAS1.
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                                                                                                                                                                                                                                                                                                                                                                            Watson SA;
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                                                                                                                                                                                                                                                                                                                                                                            Michaeli D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                             /note= "C-terminal amide"
                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Figure 1B; 37pp; English.
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                                                                                                                                                                                                                                                                                                                96US-0011411.
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                                           Carboxy-amidated gastrin-1
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            13-MAR-1998 (first entry
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                                                                                                                                                                                                                                                                                                                                                                            Grimes S,
                                                                                                                                                                                                                                                                                                                                              (APHT-) APHTON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-415075/38.
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 AA;
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                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                   07-FEB-1997;
                                                                                                                                                                                                                                                                                                                08-FEB-1996;
                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                          WO9728821-A1
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                                                                                                                                                                                                                                                                                                                                                                          Gevas PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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The sequence represents a synthetic biotinylated peptide substrate for human Janus kinase 3 (JAK3). The invention relates to the use of JAK37TAT (Janus kinase/Asignal transducer and activator of transcription) inhibitors other than debromohymenialdisine (DBH) and hymenialdisine (H) for inhibiting the progression or the likelihood of developing diseases involving cartilage degradation, and for requiating the expression or the likelihood of the expression of pro-inflammatory agents or cytckines in a chondrocyte, and cartilage degrading enzymes in a cell. A JAK3/STAT inhibitor of the invention is useful for inhibiting progression or likelihood of developing osteoarthritis or rheumatoid arthritis. The inhibitor of the invention is useful for inhibiting progression or likelihood of the cuseful for treating other JAK/STAT-mediated disorders, and including T cell-mediated disorders include human T cell-mediated disorders include human T cell-mediated disorders include human T cell eleukaemia/lymphoma virus (HTLV)-1, Sdzory's syndrome, c-abl transformation, natural killer-like T cell lymphomas (NK-like tumours) and graft-vs-host disease; cytokine hypersensitivity disorders include and graft-vs-host disease; cytokine hypersensitivity disorders include and graft-vs-host disease; cytokine hypersensitivity disorders include acute lymphocytic and lymphoblastic leukaemias and lymphomas include acute lymphocytic and lymphoblastic leukaemias and lymphoglastic leukaemias of myeloid origin. DBH and He is the signification in which JAK3 plays a role in the infinitiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of inhibitors of Janus kinase/signal transducers and activators of transcription for inhibiting onset and progression of degenerative joint diseases or disorders such as osteoarthritis, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumourigenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 53; DB 22; Best Local Similarity 100.0%; Pred. No. 0.033; Matches 9; Conservative 0; Mismatches 0;
                                                                             "Glu is biotinylated"
                                                                                                                   amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are useful as therapeutic agents in
in the initiation or progression of
                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Page 18; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
AAB91246
1D AAB91246 standard; Peptide; 17 AA
XX
AC AAB91246;
XX
DT 22-JUN-2001 (first entry)
XX
                                                                                                                   "Phe is
                                                                                                                                                                                                                                                                               24-JAN-2000; 2000US-0177872.
28-NOV-2000; 2000US-0723490.
                                                                                                                                                                                                                                       22-JAN-2001; 2001WO-US02033
                                                                                                                       /note=
                                                                             /note=
                                                                                                                                                                                                                                                                                                                                          (GENZ ) GENZYME CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-465338/50
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                                       Key
Modified-site
                                                                                                Modified-site
                                                                                                                                                                                                 26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                  Vasios G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Kauvar LM;

Cairns N,

Synthetic.

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The present invention relates to detecting addition or removal of a phosphate group to or from a substrate. The method involves contacting a luminescent peptide with a binding partner that binds specifically of a phosphorylated peptide without regard to the particular amino acid sequence of the peptide. The method is useful for detecting phosphorylation and dephosphorylation modifications of proteins,
                                                                                                                                                                                                                                                                                                                                              Assay for detecting phosphorylation and dephosphorylation modification of proteins by contacting luminescence peptide with a binding partner and measuring change in luminescence polarization .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      including kinases and phosphatases. The methods can be used to study the kinase activity of different receptors e.g. the insulin receptor and to find agonists and antagonists of these receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 53; DB Pred. No. 0.03 Mismatches
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                                                                                                                                                                                                                                                                      Lee SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein kinase A (PKA) substrate #3
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                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 70; Page 70; 89pp; English.
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                                                                                                                                                      99US-0138438.
99US-0349733.
                                                                                                                                     99US-0138311.
                                                                                                                                                                                                                                                                      Sportsman JR, Hoekstra MF,
                                                                                               2000WO-US16025
                                                                                                                                                                                            2000US-0200594
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                                                                                                                                                                                                                                   (LJLB-) LJL BIOSYSTEMS INC
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                         WPI; 2001-091201/10.
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                       WO200075167-A2.
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Modified-site
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                                                                                               09-JUN-2000;
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                                                                                                                                   09-JUN-1999;
10-JUN-1999;
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                                                                                                                                                                          08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-2002.
                                                          14-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU76504;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidy) and malelmido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3:50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.

Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half infa and specificity as bonding to large molecules decreases in the MB90823 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                     Protection, endogenous therapeutic peptide, peptidase, conjugation; blood component, modification; succinimidy1; maleimido group, amino; hydroxy1; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                     Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dength 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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O
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Pred. No. 0.033;
Gastrin releasing peptide (GRP) SEQ ID NO:422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 336; 733pp; English.
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99US-0153406.
99US-0159783.
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ilarity 100.08
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KS2-peptide substrate
                                                                                                                                                                                                                                                                                                                                                                (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 AA;
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                                                                                                                                                                      WO200069900-A2.
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EGPWLEEEE
                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                      17-MAY-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                           15-OCT-1999;
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                                                                                                                                                                                                           23-NOV-2000
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.. 0

Gaps

.. 0

0; Indels

98US-0174216

16-0CT-1998;

Phosphorylation; kinase; insulin

AAB59273;

RESULT 12 AAB59273

g

Sequence

Matches

Unidentified

(PHAR-) PHARMACOPEIA INC

DB 22; Length 17; 0.033;

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The invention relates to a reagent (I) for incorporation of a phosphorylation site by reaction with a reactive side chain of a compound to be phosphorylated. (I) comprises a structure A-B-C, where A is a moity that is specifically reactive with a reactive side chain, C is a petide sequence comprising kinase substrate, and B is a linking moiety selected from any one of the 19 compounds given in the specification e.g. N-gamma-maleimidobutyryloxy-succinamide ester. (I) is useful for phosphorylation, by reacting (I) with a compound to be phosphorylated compounds a protein or polypeptide) and then phosphorylating the resulting production or polypeptide) and then phosphorylating conditions comprising 32P-phosphorylating of synthesised proteins without the comprising 32P-phosphorylating already synthesised proteins, without the need to carry out recombinant methods to incorporate an amino acid sequence. The method is highly adaptable and can be used to phosphorylate or avoids production of proteins having an inaccessible kinase substrate sequence as can result from known recombinant methods. Introduction of sequence compliant method is possible merely by increasing the ratio of reagent to protein, and the method allows labeled increasing the ratio of reagent to protein site in protein's function or become phosphorylating does not interfere with the protein's function or pecome compliant in accessible as a result of protein folding. The method allows labeled compounds that have a higher specific activity that is cormally obtained with recombinant methods. The protein sequence cormally obtained with recombinant methods are useful in examples to protein folding. The present sequence cormally obtained with recombinant methods as the present sequence cormally obtained with recombinant methods. The present sequence cormally obtained with recombinant methods and the method in examples that demonstrate the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine-extended gastrin-17; gastrointestinal tumour; immunogen; colorectal adenocarcinoma; antibody; progastrin; cholecystokinin B; anti-gastrin-17; anti-617.
                                                                                                        Reagent for phosphorylating a compound, comprises a moiety that is specifically reactive with reactive site chain of the compound, a linking moiety and a peptide sequence comprising kinase substrate
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 53; DB 23; Length 17; 100.0%; Pred. No. 0.033; 1ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                              Disclosure; Column 8; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW24397 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycine-extended gastrin-17.
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                    Glickman JF;
                                                               WPI; 2002-194620/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-1997
                      Inglese J,
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The present sequence represents glycine-extended gastrin-17. Treatment of glycine-extended gastrin-17 (Gl7-Gly)-dependent gastrointestinal tumours comprises administering an anti-gastrin 7 (anti-G17) immunogenic comprosition. Anti-G17 immunogens raise antibodies which bind both the amidated and glycine-extended forms of Gl7. Neutralisation of progastrin Gl7-Gly prohormone by the antibodies inhibits the growth of tumour cells dependent on progastrin Gl7-Gly as growth stimulator or adenocarcinomas in humans. This novel method is non-invasive, selectively reversible, does not damage normal tissue, does not require frequent repeated treatments and does not cross the blood brain
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helper T cell epitope; universal immune stimulator; invasin; hapten;
                                                                            Treatment of glycine-extended gastrin-17-dependent gastrointestinal tumours - using anti-G17 immunogenic composition, especially for treatment of colorectal adenocarcinomas
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic luteinising hormone releasing hormone peptide(s) that suppress LHRH activity in males and females
                                                                                                                                                                                                                                                                                                                                                                    Length 18;
                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                            Watson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gastrin; peptic ulcers; gastrin-stimulated tumours
                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 53; DB 18; 100.0%; Pred. No. 0.035;
                          Michaeli D,
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                  Example 1; Figure 1A; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR62740 standard; peptide; 12 AA.
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                          Karr SL,
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                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity luv...
(APHT-) APHTON CORP.
                                                  WPI; 1997-415075/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-357910/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LADD/) LADD A E. (WANG/) WANG C Y. (ZAMB/) ZAMB T.
                                                                                                                                                                                                                                                                                                                                      18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     1 EGPWLEEEE 9
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EGPWLEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gastrin hapten.
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                                                                                                                                                                                                                                                                                                                                       Sequence
                         Gevas
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AAR62740
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Synthetic immunogenic peptides are provided in which a universal immune stimulator is linked to a peptide or protein hapten containing B cell and/or cytofoxic T lymphocyte epitopes, giving a product which causes potent immune responses to the coupled peptide or protein. The stimulator consists of (A) a promiscuous helper T cell epitope (Th) which elicits an immune response to the coupled peptide in members of a heterogeneous population expressing diverse HLA phenotypes, and (B) an adjuvant peptide sequence from the invasin protein of Yersinia. Spacer amino acid sequence from the invasin protein of Yersinia. Components. When the hapten is LHRH, then optionally the invasin domain can be omitted from the immune stimulator component.

The present sequence is an example of a gastrin hapten which can be bound to the immune stimulater furmant avaccine for treating to be peptic ulcer disease or gastrin-stimulated tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.3%; Score 50; DB 15; Length 12; 88.9%; Pred. No. 0.071; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.9 Matches 8; Conservative
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Gaps ó;

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1 EGPWLEEEE 9

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February 5, 2003, 09:49:21 ; Search time 6.85714 Seconds
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29.097 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/RCG_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129505 seqs, 22169297 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                 US-09-700-329-1
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                                                                                                                OM protein - protein search,
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                                                                                                                                                                                                                                                                                Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 4, Appli	Sequence 1205, Ap	Sequence 16, Appl	Sequence 4, Appli	_`	2, 1	Sequence 4, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 4, Appli	Sequence 5, Appli	Sequence 6, Appli	'n	Sequence 14, Appl	Sequence 34, Appl	Sequence 7, Appli	Sequence 26, Appl	Sequence 18, Appl	Sequence 20, Appl
ID	US-10-192-257-4	0 US-09-764-864-1205	US-10-021-811-16	US-10-021-811-4	US-10-021-811-14	US-09-956-993-2	US-09-956-993-4	0 US-09-838-561-8	0 US-09-816-760-8	0 US-09-757-049A-4	0 US-09-757-049A-5	0 US-09-757-049A-6	0 US-09-912-962-13	0 US-09-912-962-14	US-10-021-811-34	0 US-09-828-648-7	US-10-004-551-26	US-10-004-551-18	US-10-004-551-20
% Query Match Length DB	16 9	182 1(62 9	179 9	221 9	317 9	369	369 10	369 10	50 口(50 11	50 11	52 10		206	99 1	261 9	525 9	525 9
% Query Match Le	90.6	75.5	71.7	71.7	71.7	71.7	71.7	71.7	71.7	8.69	8.69	8.69	69.8	8.69	8.69	67.9	67.9	67.9	67.9
Score	48	40	38	38	38	38	38	38	38	37	37	37	37	37	37	36	36	36	36
Result No.	-	7	e	4	S	9	7	80	g	10	11	12	13	14	15	16	17	18	19

3,27	Sequence 28, Appl Sequence 76, Appl Sequence 96, Appl
9 US-10-004-551-22 9 US-11-004-551-14 9 US-10-004-551-14 9 US-10-004-551-14 9 US-10-009-567B-47 1 US-09-864-161-47725 9 US-10-018-118A-36 9 US-10-021-811-62 9 US-10-021-811-62 9 US-10-021-811-64 10 US-09-443-704-16 10 US-09-443-704-16 10 US-09-118A-18 10 US-09-443-704-16 10 US-09-443-704-16 10 US-09-443-704-16 10 US-09-443-704-16 10 US-09-443-704-18 10 US-09-443-704-18 10 US-09-931-087A-1 10 US-09-931-087A-1 10 US-09-931-087A-22 10 US-09-931-087A-23	9 US-10-021-811-28 10 US-09-751-100B-76 10 US-09-751-100B-96
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ALIGNMENTS

RESULT 1

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Sequence 4, Application US/10192257

Sequence 4, Application US/10192257

Publication No. US20030021786A1

GENERAL INFORMATION:
APPLICANT: Aphton Corporation

TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Condit

TITLE OF INVENTION: Liver, Lung and Esophagus

FILE REFERENCE: 1102865-0057

CURRENT APPLICATION NUMBER: US/10/192,257

CURRENT FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: US 60/303,868

PRIOR FILING DATE: 2001-07-09

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 16

THE CORPORATION OF 10 NO 10
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Patent No. US20020132753A1;
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies;
FILE REFERENCE: PTZ23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 16;
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. 0.038;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa-pyroglutamic acid
US-10-192-257-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 90.6%; Sc
Best Local Similarity 100.0%; P
Matches 8; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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2 GPWLEEEE 9
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US-09-764-864-1205
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GENERAL INFORMATION:

A PAPLICANT: WEIL.

ITILE OF INVENTION:

TITLE OF INVENTION: MOLECULES ENCODING HUMAN ENZYME, AND USES THEREOF

TITLE OF INVENTION: MOLECULES ENCODING HUMAN ENZYME, AND USES THEREOF

FILE REFERENCE: CLOOLIBAIDIV

CURRENT APPLICATION NUMBER: US/09/956,993

CURRENT FILING DATE: 2001-09-21
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US-10-021-811-14
Sequence 14, Application US/10021811
Sequence 14. Application US/10021811
Sequence 14. Application US/10021811
Sequence 14. Application Vo. US20030024007A1
SENERAL INFORMATION:
APPLICANT: Rend, Tiwen
APPLICANT: Weell, Joan
TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
FILE REFERENCE: B81294 US NA
CURRENT APPLICATION NUMBER: US/10/021,811
SPRIOR APPLICATION NUMBER: 60/110,609
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
                                                                    APPLICANT: Cardon, Rebecca E.
APPLICANT: Fang, Yiwen
APPLICANT: Fang, Yiwen
APPLICANT: Godell, Joan
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
FILE REFERENCE: BB1294 US NA
CURRENT FILING DATE: 2001-12-14
PRIOR PPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 9; Length 179;
Pred. No. 17;
3; Mismatches 1; Indels
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Pred. No. 21;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.78;
55.68;
                               Publication No. US20030024007A1
GENERAL INFORMATION:
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55.68;
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SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 221
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Best Local Similarity 55.6
Matches 5; Conservative
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US-10-021-811-14
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Best Local Similarity
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10 KGPWTEQED 18
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3 KGPWTEQED 11
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LOCATION: (177)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1205
                                                                                                                                                                                                                                           LOCATION: (23)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Sequence 16, Application US/10021811

Publication No. US20030024007A1

GENERAL INFORMATION:

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Fang, Yiwen

APPLICANT: Fang, Yiwen

APPLICANT: Weng, Zude

TITLE OF INVENTION: Plant Myb Transcription Factor Homologs

FILE REFERENCE: BAL294 US NA

CURRENT APPLICATION NUMBER: US/10/021,811

CURRENT FILING DATE: 1998-December-02

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Microsoft Office 97

SEQ ID NO 16

LENGTH: 62

TENGTH: 62
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO.1205
LENGTH: 182
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Pred. No. 8.2;
1; Mismatches 0; Indels
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Pred. No. 6;
3; Mismatches 1; Indels
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85.7%;
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55.68;
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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10 KGPWTEQED 18
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; LOCATION: (59)
US-10-021-811-16
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                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
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US-10-021-811-4
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NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 50
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                   Query Match 71.7
Best Local Similarity 100.
Matches 6; Conservative
                                                                       ; ORGANISM: Homo sapiens US-09-838-561-8
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47 GPWLEE 52
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US-09-757-049A-4
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LENGTH: 369
   LENGTH: 369
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US-09-816-760-8
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Fatent No. US20020164733A1
GENERAL INFORMATION:
TITLE OF INVENTION:
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GENERAL INFORMATION:
APPLICANT: Mayers, Rachel
APPLICANT: Mayers, Rachel
APPLICANT: Mayers, Rachel
APPLICANT: Milliam James
APPLICANT: Milliam Mark
APPLICANT: Midolph-Owen, Laura A.
APPLICANT: Gimeno, Ruth
TITLE OF INVENTION: 32142, 21481, 25964, 21686, NOVEL DEHYDROGENASE
TITLE OF INVENTION: MOLECULES AND USES THEREFOR
FILE REFERENCE: MILLIAGE AND USES THEREFOR
CURRENT APPLICATION NUMBER: US/09/818,561
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 09/814,955
PRIOR APPLICATION NUMBER: 09/814,955
PRIOR FILING DATE: 2000-08-08
PRIOR FILING DATE: 2000-08-08
PRIOR FILING DATE: 2000-08-08
PRIOR FILING DATE: 2000-08-08
SPRIOR FILING DATE: 2000-08-08
SPRIOR FILING DATE: 2000-08-08
SPRIOR FILING DATE: 2000-08-08
SOFTWARE: PARENTING NUMBER: 60/192,002
SOFTWARE: PARENTIN VOS: 16
SSEQ ID NO 8
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30;
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                                                             NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 317
                                                                                                                                                                                                                                                                                                                                   Score 38;
Pred. No.
PRIOR APPLICATION NUMBER: 09/816,088 PRIOR FILING DATE: 2001-03-26
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100.0%;
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100.0%;
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Best Local Similarity 100.
Matches 6; Conservative
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US-09-956-993-4
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US-09-956-993-2
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Best Local Similarity
Matches 6; Conserv
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47 GPWLEE 52
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US-09-956-993-4
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APPLICANT: BERNSTEIN, Harold S.

APPLICANT: BERNSTEIN, Harold S.

APPLICANT: COUGHLIN, Shaun R.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING CELL CYCLE

TITLE OF INVENTION: PROGRESSION

FILE REPERENCE: UCSP-020/020S

CURRENT APPLICATION NUMBER: US/09/757,049A

CURRENT FILING DATE: 1908-09-108

PRIOR PILING DATE: 1998-09-108

PRIOR APPLICATION NUMBER: US 60/060,688
                                                             Gaps
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Pred. No. 34;
0; Mismatches 0; Indels
              DB 10; Length 369; 34;
                                                          Indels
                                                                                                                                                                                                                                                                                                                                               APPLICANT: COOK, William James
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Laura A.
ITLE OF INVENTION: 32142, 21481, 25964, 21686, N
ITLE OF INVENTION: MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-134CP
71.7%; Scc...
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/816,760
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 09/634,955
PRIOR FILING DATE: 2000-08-08
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTUM VOICE: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 4, Application US/09757049A ; Patent No. US20020127702A1
                                                                                                                                                                                                                                                           Sequence 8, Application US/09816760
Patent No. US20020015232A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel
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100.08; Pre
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RESULT 13
US-09-912-962-13
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                                                                                                                                                                        Sequence 5. Application US/09757049A
Fatent No. US20020127702A1
GENERAL INFORMATION:
APPLICANT: BERNSTEIN, Harold S.
APPLICANT: COUGHLIN, Shaun R.
TITLE OF INVENTION: PROGRESSION
FILE REFERENCE: UCSF-020/02US
CURRENT APPLICATION NUMBER: US/09/757,049A
CURRENT FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIN Ver. 2/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09757049A

Patent No. US20020127702A1

GENERAL INFORMATION:
APPLICANT: BERNSTEIN, Harold S.
TITLE OF INVENTION: PROGRESSION
TITLE OF INVENTION: PROGRESSION
FILE REFERENCE: USF-020/2018
CURRENT APPLICATION NUMBER: US/09/757,049A
CURRENT FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-22
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 50
                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 10; Length 50; Pred. No 7; 3; Mismatches; 1; Indels
Score 37; DB 10; Length 50;
Pred. No. 7;
                                  1; Indels
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                                 3; Mismatches
69.8%;
55.6%;
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55.6%;
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 69.8
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRCANISM: Homo sapiens
US-09-757-049A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
               Best Local Similarity
Matches 5; Conserv
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2 KGPWTKEED 10
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2 KGPWTKEED 10
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2 KGPWTKEED 10
                                                                  1 EGPWLEEEE 9
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US-09-757-049A-6
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US-09-757-049A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 5
LENGTH: 50
 Query Match
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                                                                                                                     Smogorzewska, Agata
TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND
DIAGNOSTIC AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND
DIAGNOSTIC AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.8%; Score 37; DB 10; Length 52; 55.6%; Pred. No. 7.3; 1: Indels 1: of 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/018,635
FILING DATE: 04-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: David A. Jackson
REGISTRATION NUMBER: 26,742
REFERRNCE/POCKET NUMBER: 600-1-142 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/912,962
FILING DATE: 25-Jul-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-912-962-13
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                                                                                                                                                                                                                                                               STREET: 411 Hackensack Avenue
                                                                       APPLICANT: de Lange, Titia
Broccoli, Dominique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Broccoli, Dominique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/09912962 Patent No. US20020076719A1 GENERAL INFORMATION:
Sequence 13, Application US/09912962 Patent No. US20020076719A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: de Lange, Titia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER
                                                                                                                                                                                                                                                                                                                                                          ZIP: 07601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                          NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                           STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                        CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
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Best Local Similarity
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3 KGPWTKEED 11
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US-09-912-962-14
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Sequence 34, Application US/10021811
Sequence 34, Application Wo. US2003024007A1
Sequence Application No. US2003024007A1
SENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Odell, Joan
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
FILE REFERENCE: BB1294 US NA
CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Microsoft Office 97
SEQ ID NO 34
LENGTH: 206
                                                                                                                          MEDIUM TIEM FORDATION
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/912,962
FILING DATE: 25-Jul-2001
FILING DATE: 15-Jul-2001
PRIOR APPLICATION NUMBER: 09/018,635
FILING DATE: 04-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: DAYLO A-FEB-1998
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
TELERAX: 201-343-1684
TELERAX: 201-343-1684
TELERAX: 201-343-1684
TELERAX: 201-343-1684
TELERAX: 133521
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARAFEISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.8%; Score 37; DB 9; Length 206; 55.6%; Pred. No. 28; Live 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 69.8%; Score 37; DB 10; Length 52; Best Local Similarity 55.6%; Pred. No. 7.3; Matches 5; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-912-962-14
                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 52 amino acids
                                                                ZIP: 07601
COMPUTER READABLE FORM:
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 69.8 Best Local Similarity 55.6 Matches 5; Conservative
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; ORGANISM: Glycine max
US-10-021-811-34
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3 KGPWTKEED 11
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16 KGPWIMEED 24
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US-10-021-811-34
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Search completed: February 5, 2003, 09:56:01 Job time : 6.85714 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

February 5, 2003, 09:46:31; Search time 11.5714 Seconds (without alignments)
74.771 Million dell updates/sec Run on:

US-09-700-329-1 53 1 EGPWLEEEE 9 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

pirl:* pir2:* pir3:* PIR_73:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	bia aastrin - Nort	rin precur			_		gastrin - sheep		gastrin precursor	MYB27 protein - Ar	little gastrin - C	deoxyhypusine synt				Ω	myb-related protei	biq qastrin fvalid	gastrin -	n nIa -	myb-related protei	probable MYB trans	ö	lass í hi	ajor	I major	I major	protein	hetical p
SUMMARIES																														
SUMM	DI	A60506	GMHUB	GMCT	A60071	GMPGB	GMDG	GMSH	JS0426	GMBO	T46166	A29541	C75119	F64401	C91080	D85925	JQ2390	T09758	GMGPB	B29541	S20350	JQ0961	A71448	C35878	A49885	E35878	A35878	B35878	S11246	T00808
	DB	7	Н	П	~	Н	Н	Н	7	-	7	N	~	7	7	7	٦	7	, - 1	7	7	Н	7	~	7	7	7	7	7	~
	Length	33	101	104	17	104	104	17	34	104	238	16	335	370	248	248	273	293	33	33	110	268	745	204	377	379	379	406	498	096
₩	Query	94.3	94.3	94.3	90.6	90.6	90.6	88.7	88.7	88.7	84.9	81.1	81.1	79.2	77.4	77.4	77.4	77.4	75.5	75.5	75.5	75.5	75.5	73.6	73.6	73.6	73.6	73.6	73.6	73.6
	Score	20	20	20	48	48	48	47	47	47	45	43	43	42	41	41	41	41	40	40	40	40	40	30	39	39	39	39	39	39
	Result No.	П		e	4	2	9	7	&	σ	10	11	12	13		15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

	myb-related transc	Myb DNA binding pr	myb-related protei	probable transcrip	N-acetylglucosamin	myb-like protein -	hypothetical prote	alpha-actinin - Ca	hypothetical prote	hypothetical prote	probable tenascin	napin nIb - rape	MJ0653 homolog AF0	conserved hypothet	SEC14 protein - ve	R2R3-MYB transcrip	
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	T51666	T49254	T03850	T51509	D82158	T48253	T26149	A48403	T26147	T41135	T09070	S26636	G69355	F69335	A37766	T45859	
	7	7	~	7	7	7	7	7	?	7	7	7	~	7	-	7	
	234	256	278	325	378	529	894	910	920	982	4006	106	189	222	301	301	
	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	8.69	8.69	8.69	8.69	8.69	
	38	38	38	38	38	38	38	38	38	38	38	37	37	37	37	37	
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

Comp. Blochem. Physiol. B 96, 239-242, 19400, K.S. Comp. Blochem. Physiol. B 96, 239-242, 1990 A,Title: Opossum (Didelphis virginiana) "little" and "big" gastrins. A,Reference number: A60506; MUID:90298616; PMID:2361360 A,Accession: A60506 A,Molecule type: protein A,Residues: 1-33 <shi> C,Superfamily: gastrin C,Keywords: amidated carboxyl end; hormone; pyroglutamic acid; sulfoprotein C,Keywords: amidated carboxyl end; hormone; pyroglutamic acid; sulfoprotein F;1-33/Product: big gastrin #status experimental <matb> F;18-33/Product: big gastrin #status carboxylic acid (GIn) #status experimental F;28/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental F;33/Modified site: amidated carboxyl end (Phe) #status experimental</matb></shi>
Ollory Match 94 38. Soore 50. DB 2. Tongth 22.

Length 33; 94.3**%**; 88.9**%**;

Gaps 0, 0; Indels Score 50; DB 2; Pred. No. 0.037; 1; Mismatches Query Match Best Local Similarity 88.9 Matches 8; Conservative

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1 EGPWLEEEE 9 :||||||||| 18 QGPWLEEEE 26 qq δλ

RESULT 2 GMHUB

Gastrin precursor [validated] - human
N;Contains: big gastrin; cryptagastrin; gastrin-17
C;Species: Box sapiens (man)
C;Species: Homo sapiens (man)
A;Reference number: A3397; MUD:84272693; PMID:6182987; PIDN:AABS9533.1; PID:g182989
R;Rato, K.; Hayashizaki, Y.; Takahashi, Y.; Himeno, S.; Matsubara, K.
Nucleic Acids Res. 11, 8197-8203, 1983
A;Title: Molecular cloning of the human gastrin gene.
A;Reference number: A93497; MUD:84169471; PMID:6324077
A;Accession: A93497
A;Molecule type: DNA

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Nicontains: big gastrin (gastrin 34); gastrin (contains) big gastrin (gastrin 34); gastrin (contains) big gastrin (gastrin 34); gastrin (contains) big gastrin (contains) big salvestris catus (domestic cat) (c) bate: 13-Jun-1983 #sequence_revision 02-Jun-1994 #text_change 20-Oct-2000 (c) bate: 13-Jun-1983 #sequence_revision 02-Jun-1994 #text_change 20-Oct-2000 (c) big salvestrin (c) big salv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Superfamily: gastrin

C.Superfamily: gastrin

C.Superfamily: gastrin

C.Steywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein

C.Steywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein

E;1-21/Domain: signal sequence #status predicted <SIG>
        F:1-21/Domain: signal sequence #status properties | #status experimental construction | #status experimental | #status expe
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A; Residues: 1-104 <KIMS
A; Cross-references: EMBL:X16582; NID:91099; PIDN:CAA34599.1; PID:91100
A; Cross-references: EMBL:X16582; NID:91099; PIDN:CAA34599.1; PID:91100
B; Agarwal, K.L.; Kenner, G.W.; Sheppard, R.C.
J. Am. Chem. Soc. 91, 3096-3097, 1969
A; Title: Feline gastrin. An example of peptide sequence analysis by mass spectrometry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Modecule type: DNA
A; Modecule type: DNA
A; Modecule type: DNA
A; Residues: 1-101 (KAR>
A; Cross-references: GB:M15958; NID:9182990; PIDN:AAA52520.1; PID:9182991
EMBO J. 14, 389-396, 1995
A; Title: Post-polyy(Glu) cleavage and degradation modified by O-sulfated tyrosine: a r
A; Reference number: S54350; MUID:95137019; PMID:7530658
                                                                                                                                                                                         ACCOSS-references: EMBL:V00511; NID:g31654; PIDN:CAA23769.1; PID:g31655
R;Rehfeld, J.F.; Johnsen, A.H.
Eur. J. Blochem. 237, 755-773, 1994
A.;Title: Identification of gastrin component I as gastrin-71. The largest possible A;Reference number: $48183; MUID:94333379; PMID:8055952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Status: preliminary
A.Molecule type: procein
A.Residues: 22-40 (REH>
R:Kariya, Y.; Kato, K.; Hayashizaki, Y.; Himeno, S.; Tarui, S.; Matsubara,
Gene 50, 345-352, 1986
A:Title: Expression of human gastrin gene in normal and gastrinoma tissues.
A.Reference number: 154006; MUID:87219893; PMID:3034736
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88.9%; Pred. No. 0.13;
Live 1; Mismatches
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A;Cross-references: GDB:119261; OMIM:137250
A;Map position: 17q-17q
A;Introns: 71/1
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Best Local Similarity
Matches 8; Conserv
                                                                          A; Molecule type: mRNA
A; Residues: 1-101 <RES>
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                      A;Cross treferences (B:X0018), ND:931648; PIDN:CAA25005.1; PID:931649
R;Haris, J. I.; Kenner, E.W.
unpublished results, cited by Gregory, R.A., and Tracy, H.J., in Gastrointestinal Hormon
A;Reference number: A94473
A;Accession: A93152
A;Accession: A9168
A;Accession: A9188
A;Accession: A4088
A;Accession: A4088
A;Accession: A4088
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A;Acce
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A Molecule type: protein
A Molecule type: protein
A; Molecules: 22-51 <HUE>
B; Higashimoto, Y.; Himeno, S.; Shinomura, Y.; Nagao, K.; Tamura, T.; Tarui, S.
Biochem. Biophys. Res. Commun. 160, 1364-1370, 1989
A; Title: Purification and structural determination of urinary NH-2-terminal big gastrin
A; Reference number: A32487; MUID:89273602; PMID:2730647
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R;Boel, E.; Vuust, J.; Norris, F.; Norris, K.; Wind, A.; Rehfeld, J.F.; Marcker, K.A.
Proc. Natl. Acad. Sci. U.S.A. 80, 2866-2869, 1983
A;Title: Molecular cloning of human gastrin cDNA: evidence for evolution of gastrin by
A;Reference number: I37408; MUID:83221503; PMID:6574456
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A; Molecule type: protein
A; Mosiques: 59-67 <HI2>
A; Experimental source: urine
A; Mocession: B32497
A; Molecule type: protein
A; Residues: 59-66 <HI3>
A; Molecule type: protein

A; Residues: 1-101 <KAT>
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A Residues: 97-104 CDES.

A Residues: 97-104 CDES.

C Superfamily: 97-104 CDES.

C Superfamily: 97-104 CDES.

C Superfamily: 97-104 CDES.

C Superfamily: 97-104 CDES.

C Reywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein c; fill-21/Domain: sugnal sequence #status predicted <PRO>

F;1-21/Domain: anino-terminal propeptide #status predicted <PRO>
F;2-56/Domain: amino-terminal propeptide #status predicted <PRO>
F;59-92/Product: pastrin #status experimental <PRO>
F;59-92/Product: gastrin #status experimental <PRO>
F;59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following F;96/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M25036; NID:g164626; PIDN:AAA31111.1; PID:g164627
R;Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.
Regul, Pept. 25, 223-233, 1989
A;Title: The constitution and properties of phosphorylated and unphosphorylated C-ter A;Reference number: A60070; MUID:89331947; PMID:2756156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.A.; Gregory, R.A.; Hardy, P.M.; Kenner, G.W.; MacLeod,
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N;Contains: big gastrin; gastrin
C;Species: Canis Lupus familiaris (dog)
C;Date: 13-Jun-1983 #sequence_revision 14-Jul-1994 #text_change 20-Oct-2000
C;Accession: B61053; A61053; JS0425; A01620; B60070
C;Accession: B61053; A61053; JS0425; A01620; B60070
Digestion 46, 99-104, 1990
A;Title: Cloning of canine gastrin cDNA's encoding variant amino acid sequences. A;Reference number: A61053; MUD:91085716; PMID:2262079
A;Accession: B61053
A;Accession: B61053
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-104 <GAN>A;Accession: B6104 <GAN>A;Accession: B6105 <ACCESSION <A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          using an oligonucleotide probe. PMID:6930858
                             A; Accession: 194473
A; Molecule type: protein
A; Residues: 59-64, HBP', 68-92 < HAR>
A; Residues: 59-64, HBP', 68-92 < HAR>
A; Note: Tyr-87 is sulfated in two-thirds of the molecules
A; Note: this peptide was extracted from the antral mucosa
B; Gregory, H.; Hardy, P. M.; Jones, D.S.; Kenner, G.W.; Sheppard,
Nature 204, 931-933, 1964
A; Title: The antral hormone qastrin.
A; Reference number: A93148
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A; Contents: annotation; synthesis
R; Agarwal, K.L.; Noyes, B.E.
Ann. N. Y. Acad. Sci. 343, 433-442, 1980
A; Title: Studies on gastrin mRNA structure
A; Reference number: I46622; MUID:80240380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 56-82 <AGA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Anderson, J.C.; Barton,
Nature 204, 933-934, 1964
                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 76-92 <GRE>
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R:Harris, J.I.; Kenner, E.W.
unpublished results, cited by Gregory, R.A., and Tracy, H.J., in Gastrointestinal Hormon
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A.Molecule type: protein

S.Superfamily: gastrin

C.Superfamily: gastrin

C.Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein

C.Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein

C.Keywords: amidated carboxyl end; pyroglutamic acid; sulfoprotein

C.Keywords: amidated carboxyl end; pyroglutamic acid; sulfoprotein

E.F.G.Yodolouci: big gastrin #$tatus experimental <br/>
AMINATORIONG carboxylic acid (Gln) (in mature form) #status experiment<br/>
F.F.Modified site: sulfate (Tyr) (covalent) (partial) #status experimental<br/>
F.92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly
                                                                                                                                                                S.; Raufman, J.P.; Straus
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C;Species: Sus scrofe domestica (domestic pig)
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 31-Dec-2000
C;Accession: A93903; B94473; A93148; IA.6522; A60070; A01618
R;Yoo, O.J.; Powell, C.T.; Agarwal, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1049-1053, 1982
A;Titles Molecular cloning and nucleotide sequence of full-length cDNA coding for A;Reference number: A93903; MUID:82174533; PMID:6951161
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C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 20-Mar-1998
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Pred. No. 0.14;
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                                                                            A Molecule type: protein
A Mesidues: 76-92 (AGA)
Residues: 76-92 (AGA)
Regul. Pept. 37, 9-13, 1992
A Mille: Cat gastrinoma and the sequende of cat gastrins.
A Reference number: A61074; MUID:92262853; PMID:1585019
A) Accession: A61074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
A; Reference number: A01621; MUID: 69206035; PMID: 5784957
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Pred. No. 0.039;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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A; Residues: 1-104 <YOO>
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76 OGPWLEEEE 84
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QGPWMEEEE
                                              A; Accession: A01621
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                 qastrin
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                                                                                                     big gastrin
N;Contains:
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JS0426
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A.Residues: 96-104 cDES>
A.Residues: 96-104 cDES>
C.Comment: Big gastrin constitutes only about 5% of antral gastrin.
C.Superfamily: gastrin
C.Superfamily: gastrin
C.Superfamily: gastrin
C.Superfamily: gastrin #status experimental cMAT>
F.1-21/Domain: signal sequence #status experimental cMAT>
F.59-92/Product: big gastrin #status experimental cMAL>
F.56-92/Product: gastrin #status experimental cMAL>
F.56/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
F.87/Modified site: sulfate (Tyr) (covalent) (partial) #status experimental
F.92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly
F.96/Binding site: phosphate (Seq) (covalent) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gastrin - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 20-Mar-1998
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 20-Mar-1998
C;Accession: A01619, Bentley, P.H.; Gregory, R.A.; Kenner, G.W.; Sheppard, R.C. Nature 219, 614-615, 1968
Nature 219, 614-615, 1968
A;Title: Isolation, structure and synthesis of ovine and bovine gastrins.
A;Reference number: A01619; MUID:68357500; PMID:5665711
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C:Keywords: amidated carboxyl end: hormone; pancreas; phosphoprotein; pyroglutamic acid;
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:12/Binding site: sulfate (Tyr) (covalent) / partial) #status experimental
F:17/Modified site: amidated carboxyl end (Phe) #status experimental
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A; Residues: 76-82, 'A', 84, 'E', 86-92 < AGA>
R; Residues: 76-82, 'A', 84, 'E', 86-92 < AGA>
R; Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.
R; Desmond, H.; Varro, A.; 1989
A; Title: The constitution and properties of phosphorylated and unphosphorylated C-termin
A; Reference number: A60070; MUID; 89331947; PMID: 2756156
A; Accession: B60070
A;Residues: 1-84,'T',86-104 <GA2>
A;Note: it is unclear whether the sequence difference results from polymorphism, multipl
R;Bonato, C.; Eng, J.; Hulmes, J.D.; Miedel, M.; Pan, Y.C.E.; Yalow, R.S.
Peptides 7, 689-693, 1986
A;Title: Sequences of gastrins purified from a single antrum of dog and of goat.
A;Reference number: JS0425; MUID:87016557; PMID:3763441
A;Accession: JS0425
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                                                                                                                                                                                                                                                                               A; Experimental source: antral mucosa
A; Note: about 10% of gastrin is sulfated
R; Agarwal, K.L.; Kenner, G.W.; Sheppard, R.C.
Experientia 25, 346-348, 1969
A;Title: Structure and synthesis of canine gastrin.
A;Reference number: A01620; MUID:69253357; PMID:5799207
A;Accession: A01620
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ilarity 77.8%; Pred. No. 0.057;
Conservative 2; Mismatches
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Best Local Similarity
7; Conserve
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A, Residues: 1-17 <AGA>
C, Superfamily: gastrin
                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 59-92 <BON>
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Best Local Similarity
Matches 7; Conserv
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1 QGPWVEEEE 9
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QGPWMEEEE
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By Gastin goat

Cipocias Court apparams hirous (domestic goat)

Cipocias Court apparams of Salatina purities from a single antum of dog and of goat.

Antities Sequence of Gastin is surjected from a single antum of dog and of goat.

Antities Sequence of Gastin is surjected from a single antum of dog and of goat.

Antuciant type: Protein

Antuciant type: Pytroidore carboxylic caid (gin) status experimental

Fill-Aproduct signification carboxylic caid (gin) status experimental

Fill-Aproduct significatin
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C; Accession: C75119
R; anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s
A; Reference number: A7501
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-335 < KAN>
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         llarity 77.8%;
Conservative
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A; Residues: 1-370 <BUL>
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Matches 7; Conserv
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deoxyhypusine synthase (EC 2.5.1.46) dysl PABO511 [similarity] - Pyrococcus abyssi (stra
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Nov-2001
           F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T46166
R;Wyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; Submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23025
A;Accession: T46166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 42/1; 85/2; 119/1
A;Note: T4D2.130
C;Superfamily: Arabidopsis myb-related protein 2; myb DNA-binding repeat homology
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C;Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata
C;Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata
C;Sacession: A3541
R;Shinomura, Y.; Eng, J.; Yalow, R.S.
Biochem. Biophys. Res. Commun. 143, 7-14, 1987
A;Title: Chinchilla "big" and "little" gastrins.
A;Title: Chinchilla "big" and "little" gastrins.
A;Reference number: A90130; MUID:87156784; PMID:3827930
A;Accession: A29541
A;Molecule type: protein
A;Residues: 1-16 <SHI>C;Superfamily: gastrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: protein T4D2.130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Mar-2000
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84.9%; Score 45; DB 2; Length 238.

Best Local Similarity 87.5%; Pred. No. 2.4;

Matches 7; Conservative 1; Mismatches 0; Indels
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87.5%; Pred. No. 0.25;
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77.8%;
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A;Molecule type: DNA
A;Residues: 1-238 <NYA>
A;Cross-references: EMBL:AL132958
A;Experimental source: cultivar
                                                                                                                                                                                                  Best_Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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76 QGPWVEEEE 84
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decyyhypusine synthase (EC 2.5.1.46) MJ0814 [similarity] - Methanococcus jannaschii decyyhypusine synthase (EC 2.5.1.46) MJ0814 [similarity] - Methanococcus jannaschii C;Species: Methers (1.5.81) Mitte, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak F,Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak F,Bult, C.J.; White, D.W.; Mirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Authors: Raine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Aterence number: A64300; MUID:96337999; PMID:8688087
A;Accession: F64401
A;Sternance number: A64300; MUID:96337999; PMID:8688087
A;Accession: F64401
A;Sternance number: A64300; MUID:96337999; PMID:8688087
A;Accession: F64401
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C;Genetics:
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: C91080
G;Accession: C91080
G;Accession: C91080
G;Becies: 18-Jul-2001
B;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, G;Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res: 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and G;A;Accession: C91080
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A;Molecule type: DNA
A;Residues: 1-248 <HAX>
A;Cross-references: GB:BA000007; PIDN:BAB37034.1; PID:g13363082; GSPDB:GN00154
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C;Keywords: hypusine biosynthesis; NAD; oxidoreductase; transferase
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81.1%; Score 43; DB 2;
77.8%; Pred. No. 7.8;
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                                              Query Match 77.4%; Score 41; DB 2; Length 248; Best Local Similarity 66.7%; Pred. No. 12; Matches 6; Conservative 2; Mismatches 1; Indels
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77.4%; Score 41; DB 2; Length 248; Best Local Similarity 66.7%; Pred. No. 12; Matches 6; Conservative 2; Mismatches 1; Indels
A;Experimental source: strain 0157:H7, substrain RIMD 0509952 C;Genetics:
A;Gene: ECS3611
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234 QGPWLSKEE 242
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234 QGPWLSKEE 242
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                              112892 seqs, 41476328 residues
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GABT_HUMAN
GABT_FELCA
GAST_MACMU
GAST_CANFA
GAST_PIG
GAST_CAPHI
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Y686_ARCFU
SC14_KLULA
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1A03_GORGO
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Score 50; DB 1; Length 33; Pred. No. 0.021; 1; Mismatches 0; Indels

h 94.3%; Similarity 88.9%; 8; Conservative

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Query Match Best Local Similarity

Best Loca Matches

RESULT 2
GAST_HUMAN STANDARD; PRT; 101 AA.
D GAST_HUMAN STANDARD; PRT; 101 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 12-JUN-2002 (Rel. 41, Last annotation update)
DE Gastrin precursor.

homo sapien mus musculu xenopus lae xenopus lae mus musculu homo sapien guillardia guillardia homo sapien homo sapien		tomi; s.	"; ce and s raction he stomach	AMILY. Sulfation.
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MYBB_HOUSE MYBB_XENLA MYBB_XENLA MYBA_HOUSE MYBA_HOWAN MYBA_CHICK FER3_PLEBO YC65_GUITH TERM_ADB40 Y972_HUMAN		virginiana (Nort ordata; Craniata Didelphimorphia;	Solsou; an S.C., iana) '1 8:239-24 ulates t cid and also stir	And intestine. SUBCELLILAR LECATION: Secreted. SIMILARITY: BELONGS TO THE GASTRIN A60506; A60506. **PPC; IPRO01651; Gastrin.** **PPC918; Gastrin; 1. ITE: PS00259; GASTRIN; 1. One: Cleavage on pair of basic residence. IDE 18 33 GASTRIN. IDE 18 33 GASTRIN. ERES 1 BIS PYRROLIDO RES 28 28 SULFATION RES 28 28 SULFATION RES 33 AA: 3856 MW: 21702RC15
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669.8 6699.8 6699.8 667.9 667.9 67.9	(Re (Re (Re	Didelphis marsupialis Bukaryota; Metazoa; Ch Mammalia; Metatheria; NOSI_TaxID=9267; [1] SEQUENCE.	ygolb; h idelphis em. Phys N: Gastr hydroch ve enzym	and intestine SUBCELLULAR LOCATION: SIMILARILY: BELONGS T SIMILARITY: BELONGS T SIMILARITY: BELONGS T SIMILARITY: BELONGS T SIMILARITY: BELONGS T
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                                                                    SEQUENCE FROM N.A. MEDLINE-87219893; PubMed-3034736; MEDLINE-87219893; PubMed-3034736; Kariya Y., Kato K., Hayashizaki Y., Himeno S., Tarui S., Matsubara K.; Expression of human gastrin gene in normal and gastrinoma tissues."; Gene 50:345-352(1986).
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-84144842; PubMed-6322186; Miborg O., Berglund L., Boel E., Norris F., Norris K., Rehfeld J.F., Marcker K.A., Vuust J.; Marcker K.A., Vuust J.; Structure of a human gastrin gene."; Proc. Natl. Acad. Sci. U.S.A. 81:1067-1069(1984).
                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning of human gastrin cDNA: evidence for evolution of gastrin by gene duplication.";
Proc. Natl. Acad. Sci. U.S.A. 80:2866-2869(1983).
                                                                                                                                                                   Ito R., Sato K., Helmer T., Jay G., Agarwal K.L.;
Structural analysis of the gene encoding human gastrin: the large
intron contains an All sequence.";
Proc. Natl. Acad. Sci. U.S.A. 81:4662-4666(1984).
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Rehfeld J.F., Johnsen A.H.;
Identification of gastrin component I as gastrin-71. The largest
possible bloactive progastrin product.";
Eur. J. Blochem. 223:765-773(1994).
                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-84169471; Pubmed-6324077;
Kato K., Hayashizaki Y., Takahashi Y., Himeno S., Matsubara K.;
"Molecular cloning of the human gastrin gene.";
Nucleic Acids Res. 11:8197-8203(1983).
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SEQUENCE FROM N.A.
MEDLINE-83221503; PubMed-6574456;
Boel E., Vuust J., Norris F., Norris K., Wind A., Rehfeld J.F.,
Marcker K.A.;
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Higashimoto Y., Himeno S., Shinomura Y., Nagao K., Tamura T.,
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Kato K., Himeno S., Takahashi Y., Wakabayashi T., Tarui
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MEDLINE-69298172; PubMed-5822140; Gregory R.A., Tracy H.J., Agarwal K.L., Grossman M.I.; "Aminoacid constitution of two gastrins isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning of human gastrin precursor cDNA.";
Gene 26:53-57(1983).
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II.";
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Bentley P.H., Kenner G.W., Sheppard
"Structures of human gastrins I and
                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-84272693; PubMed-6087340;
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            sapiens (Human).
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                                             NCBI_TaxID=9606;
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                                                                         secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stomach
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GASTRIN 52 (POTENNIAL).
BIG GASTRIN (GASTRIN 34) (COMPONENT II).
GASTRIN (GASTRIN 17) (COMPONENT III).
PYRROLIDONE CARBOXYLIC ACID.
PYRROLIDONE CARBOXYLIC ACID.
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PTM: TWO DIFFERENT PROCESSING PATHWAYS PROBABLY EXIST IN ANTRAL G-CELLS. IN THE DOMINANT PATHWAY PROGASTRIN IS CLEAVED AT THREE SITES RESULTING IN TWO MAJOR BIOACTIVE GASTRINS, GASTRINS, GASTRIN GASTRIN-17. IN THE PUTATIVE ALTERNATIVE PATHWAY, PROGASTRIN MAY BE PROCESSED ONLY AT THE MOST C-TERMINAL DIBASIC SITE RESULTING IN THE SYNTHESIS OF GASTRIN-71.

SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
Zollinger-Ellison tumour tissue.";
Gut 10:603-608(1969).
-!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00259; GASTRIN; 1.
Hormone; Cleavage on pair of basic residues; Amidation; Sulfation;
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AMIDATION (G-93 PROVIDE AMIDE GROPHOSPHORYLATION (BY SIMILARITY).
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Pred. No. 0.068;
1; Mismatches (
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01-NOV-1991 (Rel. 20, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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EMBL, X00183; CAA25006.1; -.
EMBL, X00183; CAA25007.1; -.
EMBL, V00511; CAA23769.1; -.
EMBL, M1558; AAA5220.1; -.
EMBL, K01254; AAB59533.1; -.
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Pfam; PF00918; Gastrin; 1.
SMART; SM00029; GASTRIN; 1.
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ilarity 88.9%;
Conservative
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PIR, A18854; A18854.
PIR, A32487.
PIR, B32487; B32487.
PIR, C32487.
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Best Local Similarity

8; Conserve
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P01354;
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Eutheria; Primates; Catarrhini; Cercopithecidae;
      Mammalia; Eutheria; Prime
Cercopithecinae; Macaca.
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15-JUL-1998 (Rel. 36,
15-JUN-2002 (Rel. 41,
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TISSUE=Antral mucosa;
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Best Local Similarity
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P01353;
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                              FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stomach
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PIR; S14401; S14401.

PIR: DrerPor, IPR001651; Gastrin.

Pfam; PF00918; Gastrin; 1.

SMART; SM00029; GASTRIN; 1.

PROSITE; PS00259; GASTRIN; 1.

PROSITE; PS00259; GASTRIN; 1.

PROSITE; PS00259; GASTRIN; 1.

PROSITE; PS00259; GASTRIN; 1.

PS00218; PS002191; Display Paction; Sulfation; Signal; Phosphorylation.

SIGNAL 1. 21.
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AMIDATION (G-93 PROVIDE AMIDE GROUP).
Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                            [2]
SEQUENCE OF 76-92.
MEDLINE=69206035; PubMed=5784957;
Agarwal K.L., Kenner G.W., Sheppard R.C.;
Peline gastrin. An example of peptide sequence analysis by mass
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SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
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                                                                                              SEQUENCE FROM N.A.

MEDLINE-92127058; PubMed=1773057;

Kim S.J., Uhm K.N., Kang Y.K., Yoo O.J.;

"Bovine and feline gastrin cDNA sequences and the amino ac nucleotide sequence homologies among mammalian species.";

DNA Seq. 1:181-187(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRROLIDONE CARBOXYLIC ACID. PYRROLIDONE CARBOXYLIC ACID.
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                            spectrometry.";
J. Am. Chem. Soc. 91:3096-3097(1969).
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GASTRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                            NCBI_TaxID=9685;
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Matches
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stomach
                          Yu J., Xin Y., Eng J., Yalow R.S.; "Rhesus monkey gastroenteropancreatic hormones: relationship to human
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                                                                                                      Fegul. Pept. 32:39-45(1991).

-!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Carnivora; Fissipedia; Canidae; Canis
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-!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
PIR; A60071; A60071.
InterPro, IPRO01651; Gastrin.
PROSITE; PS00259; GASTRIN; 1.
Hormone; Amidation; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Antral mucosa;
MEDLINE-91085716; PubMed-2262079;
Gantz I., Takeuchi T., Yamada T.;
"Cloning of canine gastrin cDNA's encoding variant amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYRROLIDONE CARBOXYLIC ACID.
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6F6E92C73611D39A CRC64;
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Pred. No. 0.024;
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Agarwal K.L., Kenner G.W., Sheppard R.C.,;
"Structure and synthesis of canine gastrin.";
Experientia 25:346-348(1969).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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MEDLINE=87016557; Pubmed=3763441;
MEDLINE=91164506; PubMed=2003150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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P04564;
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Best Local
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                                                                                            and increases blood circulation and water secretion in the stomach and intestine.
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Agarwal K.L., Noyes B.E.;
Astudies on gastrin mRNA structure using an oligonucleotide probe.";
Ann. N.Y. Acad. Sci. 343:433-442(1980).
           Desmond H., Varro A., Young J., Gregory H., Nemeth J., Dockray G.J., "The constitution and properties of phosphorylated and unphosphorylated C-terminal fragments of progastrin from dog and
                                           ferret antrum.";
Regul. Pept. 25:223-233(1989).
-!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction
                                                                                                                                                      InterPro; IPR001651; Gastrin.
Pfam; PF00918; Gastrin: 1.
PRARTY; SW00029; GASTRIN; 1.
PROSTIE; PS00259; GASTRIN; 1.
Hormone; Cleavage on pair of basic residues; Amidation; Sulfation;
                                                                                                                                                                                                                                                                              SULFATION (PARTIAL).
AMIDATION (G-93 PROVIDE AMIDE GROUP).
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-82174533; Pubmed-6951161; Yoo O.J., Powell C.T., Agarwal K.L.; Molecular cloning and nucleotide sequence of full-length of cDNA coding for porcine gastrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 76-92.
Gregory H., Hardy P.M., Jones D.S., Kenner G.W., Sheppard R.C.;
"The antral hormone gastrin.";
Nature 204:931-933(1964).
                                                                                                                                                                                                                                                                                                                                                                                ;
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    -!- SUBCELLULAR LOCATION: Secreted.
    -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
PIR; JS0425; GMDG.

                                                                                                                                                                                                                                                                                                                                                          Score 48; DB 1; Length 104;
                                                                                                                                                                                                                                                        PYRROLIDONE CARBOXYLIC ACID. PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                  BIG GASTRIN (GASTRIN 34).
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUN-2002 (Rel. 41, Last annotation update)
Gastrin precursor.
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2; Mismatches
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MEDLINE-89331947; PubMed-2756156;
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92
59
76
87
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
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P01351;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Anderson J.C., Barton M.A., Gregory R.A., Hardy P.M., Kenner G.W., McLeod J.K., Preston J., Sheppard R.C., Morley J.S.;
"Synthesis of gastrin.";
Nature 204:933-934(1964).

-!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stomach
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MEDLINE-8701655; pubmed=3763441;
Bonato C., Eng J., Hulmes J.D., Miedel M., Pan Y.-C.E., Yalow R.S.;
"Sequences of gastrins purified from a single antrum of dog and of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00259; GASTRIN; 1. Hormone; Cleavage on pair of basic residues; Amidation; Sulfation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID.
SULEATION (IN 68 OF THE CHAINS).
AMIDATION (G93 PROVIDE AMIDE GROUP).
PHOSPHORYLATION (BY SIMILARITY).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
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                                                                                                                                                                                             and intestine.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.15;
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InterPro; IPR001651; Gastrin.
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NCBI_TaxID=9925;
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QGPWMEEEE 84
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CONFLICT
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European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stomach
           contraction
in the stomach
                                                                                                                                                                                                                          Gaps
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MEDLINE=68357500; PubMed=5665711;
Agarwal K.L., Beacham J., Bentley P.H., Gregory R.A., Kenner G.W.,
Sheppard R.C., Tracy H.J.;
"Isolation, structure and synthesis of ovine and bovine gastrins.";
Nature 219:614-615(1968).
                                                                                                     pair of basic residues; Amidation; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92127058; PubMed-1773057; Kim S.J., Uhm K.N., Kang Y.K., Yoo O.J.; Bovine and felline gastrin cDNA sequences and the amino acid and nucleotide sequence homologies among mammalian species."; DNA Seq. 1:181-187(1991).
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                                      SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
                                                                                                                                                                                                 Score 47; DB 1; Length 34; Pred. No. 0.071;
                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                       0; Indels
estive enzymes. It also stimulates smooth muscle increases blood circulation and water secretion intestine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lund T., Olsen J., Rehfeld J.F.; "Cloning and sequencing of the bovine gastrin gene."; Mol. Endocrinol. 3:1585-1588(1989).
                                                                                                                                                                              67501111E76D0CF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                     104 AA
                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                         SULFATION
                                                                                                                                                                     AMIDATION
                                                                                                                           GASTRIN.
                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90114160; PubMed=2608050;
                                                                                                                                                                                                                                                                                                                                         (Rel. 01, Created)
                                                        PIR; JS0426; JS0426.
InterPro; IPR001651; Gastrin.
Pfam; PF00918; Gastrin; 1.
PROSITE; PS00259; GASTRIN; 1.
Hormone; Cleavage on pair of F.
                                                                                                                                                                                                 88.78;
77.88;
                                                                                                                                                                              3903 MW;
                                                                                                                                                                                                            Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                    STANDARD;
        digestive enzymes.
                                                                                                                                                                                                                                                                                                                                                  l (Rel. 20, I
2 (Rel. 41, I
                                                                                                                                      \frac{1}{29}
                                                                                                                                                                                                                                                                                                                                                                                                                          Bovidae, Bovinae, Bos
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                            taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       Gastrin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    intestine.
                                                                                                                                                                             34 AA;
                                                                                                                                                                                                                                                        :|||:||||
18 QGPWVEEEE 26
                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                  GAST_BOVIN S:
P01352; Q28114;
21-JUL-1986 (Rel
01-NOV-1991 (Rel
15-JUN-2002 (Rel
                                                                                                                          18
18
29
34
                                                                                                                                                                                                                                           1 EGPWLEEEE
                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus
Eukaryota;
                                                                                                                                  MOD_RES
MOD_RES
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                   Query Match
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the Euro
                                                                                                                           PEPTIDE
                                                                                                               PEPTIDE
                                                                                                                                                                                                                                                                                                          GAST_BOVIN
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                                                                                                                                                                                                                                                                                               RESULT 8
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stomach and intestine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 76-92.
MEDLINE=68357500; PubMed=5665711;
Agarwal K.L., Beacham J., Bentley P.H., Gregory R.A., Kenner G.W.,
Sheppard R.C., Tracy H.J.,
"Isolation, structure and synthesis of ovine and bovine gastrins.";
Nature 219:614-615(1968).
                                                                                                                                                                                                00918; Gastrin; 1.
M00029; Gastrin; 1.
PS00259; Gastrin; 1.
Cleavage on pair of basic residues; Amidation; Sulfation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                           PROVIDE AMIDE GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDIANE-9818286; PubMed=9522119; MEDLINE-9818286; PubMed=9522119; Moore C., Jie R., Shulkes A., Baldwin G.S.; "Molecular cloning and sequence of the ovine gastrin gene."; DNA Seq. 8:39-44(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 1; Length 104; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                               PYRROLIDONE CARBOXYLIC ACID. PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                             GASTRIN (GASTRIN 34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         A -> L (IN REF. 1).
N -> T (IN REF. 1).
N -> T (IN REF. 1).
E -> G (IN REF. 1).
S -> G (IN REF. 1).
S -> M (IN REF. 1).
E -> G (IN REF. 1).
S -> M (IN REF. 1).
S -> M (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                     SULFATION (PARTIAL).
AMIDATION (G-93 PROV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 AA.
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                                                                                                                                                                                                                                                                                                                               GASTRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                    PIR; S14400; S14400.
InterPro; IPR001651; Gastrin.
Pfam; PF00918; Gastrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11573 MW;
                                                                                            EMBL; M31657; AAA30537.1; -. EMBL; X16581; CAA34598.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                               Signal; Phosphorylation.
                                                                                                                                                                                                                                                                                                           Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 AA;
                                                                                                              EMBL; X16581; CAA:
PIR; B01619; GMBO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gastrin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EGPWLEEEE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9940;
                                                                                                                                                                                                          SMART; SM00029;
PROSITE; PS00259
                                                                                                                                                                                                                                                                                                           :|||:||||
76 QGPWVEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAST_SHEEP
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DYS OR PAB051
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Q9V0N5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heilig R.;
                                                                                                                                                                                                 MOD_RES
SEQUENCE
                                                                                                                 SIGNAL
                                                                                                                                       PEPTIDE
MOD_RES
MOD_RES
MOD_RES
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                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                            RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stomach
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                  Pfam; PF0018; Gastrin; 1.
SWART: SW00029; Gastrin; 1.
PROSITE; PS00259; GASTRIN; 1.
Hormone; Cleavage on pair of pasic residues; Amidation; Sulfation; Signal; Phosphorylation.
SIGNAL
                                                                                                                                                                                                                                               GASTRIN.

PYRROLIDONE CARBOXYLIC ACID.

PYRROLIDONE CARBOXXLIC ACID.

SULFATION (PARTIAL).

AMIDATION (G-93 PROVIDE AMIDE GROUP).

POSPHORYLATION (BY SIMILARITY).

624063D4B5CE5AFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Unique progastrin processing in equine G-cells suggests marginal tyrosyl sulfotransferase activity.";
Eur. J. Biochem. 255:432-438(1988).
-i- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBL_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98380242; PubMed-9716385;
Johnsen A.H., Sandin A., Rourke I.J., Bundgaard J.R., Nilsson G.,
Rehfeld J.F.;
                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted. SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
SUBCELLULAR LOCATION: Secreted. SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
                                                                                                                                                                                                                                                                                                                                           DB 1; Length 104;
                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                     BIG GASTRIN (GASTRIN 34).
                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                  Score 47; Db 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 AA
                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                    11532 MW;
                                                                                                                                                                                                                                                                                                                                        88.7%;
77.8%;
                                                                                                                              EMBL; U92801; AAB51307.1; -.
                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Equus caballus (Horse).
                                                                                                                                                                                                                           21
92
92
76
92
92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Antral mucosa;
                                                                                                                                                                                                                                                                                                                     104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gastrin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intestine
                                                                                                                                           PIR; A01619; GMSH.
                                                                                                                                                                                                                                                                                                                                                                                                                76 OGPWVEEEE 84
                                                                                                                                                                                                                                                                                                                                                                                          1 EGPWLEEEE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAST_HORSE
P55885;
                                                                                                                                                                                                                                                                                 MOD_RES
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                               PEPTIDE
MOD_RES
MOD_RES
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GAST_HORSE
                                                                                                                                                                                                                                                                                                                                                                  Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration harwest the Swiss Institute of Bioinformatics and the EMBL outstation -
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           structure and evolution.";
submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the NaD-DEPENDENT OXIDATIVE CLEAVAGE OF
FUNCTION: CATALYZES THE NAD-DEPENDENT OXIDATIVE CLEAVAGE OF
SPERMIDINE AND THE SUBSEQUENT TRANSFER OF THE BUTYLAMINE MOIETY OF
SPERMIDINE TO THE EPSILON-AMINO GROUP OF A SPECIFIC LYSINE RESIDUE
OF THE BIF-5A PRECURSOR PROTEIN TO FORM THE INTERMEDIATE
DEOXYHYPUSINE RESIDUE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID (POTENTIAL). PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                         SULFATION (PARTIAL).
AMIDATION (G-96 PROVIDE AMIDE GROUP).
PHOSPHORYLATION (BY SIMILARITY).
104166CAABSC234F CRC64;
                                                                                                                                                                                         PROSITE; PS00259; GASTRIN; 1.
Hormone; Cleavage on pair of basic residues; Amidation; Sulfation;
Signal; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- CATALYTIC ACTIVITY: [eIF5A precursor] -1ysine + spermidine = [eIF5A-precursor] -1ysine + spermidine -:- COFACTOR: NAD (BY SIMILARITY).
-:- COFACTOR: NAD (BY SIMILARITY).
-:- PATHWAY: Hypusine biosynthesis; first step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                    BIG GASTRIN (GASTRIN 34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Probable deoxyhypusine synthase (EC 2.5.1.46) (DHS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46; DB 1;
No. 0.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46;
                                                                                                                                                                                                                                                                                                                                GASTRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
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InterPro; IPR002773; DS.
Pfam; PF01916; DS; 1.
ProDom; PD007730; DS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11884 MW;
                                                                                                          InterPro; IPR001651; Gastrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.8%;
                                                                                    EMBL; Y09440; CAA70590.1; -.
                                                                                                                                      Pfam; PF00918; Gastrin; 1.
SMART; SM00029; GASTRIN; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                      9999999
9999999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-GE5 / Orsay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGPWLEKEE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=29292;
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Gaps

0;

Indels

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Mismatches

2;

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6; Conservative
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Q96PE6;
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SEQUENCE
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ZN_FING
ZN_FING
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Matches
          Matches
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                                                                                                                                                 SEQUENCE FROM N.A.

WEDLINE-96337999, bubMed-8688087;

AM EDLINE-96337999, bubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Rerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Relich C.I.,

A Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

A Cotton M.D., Roberts K.M., Hust M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

Complete genome sequence of the methanogenic archaeon, Methanococcus

Tomplete genome sequence of the methanogenic archaeon, Methanococcus

Tomplete genome sequence of the methanogenic archaeon, Methanococcus

Tomplete genome sequence of the Subsection Transfer of THE BUTYLAMINE MOIETY OF

Spermidine TO THE EDSIGNO-AMINO GROUP OF A SPECIFIC LYSINE RESIDUE

DEOXYHYPUSINE RESIDUE (MY SIMILARITY)

C.I. CATALYTIC ACTIVITY: [eIFSA-Precursor]-lysine + spermidine =

GIETSA Precursor]-deoxyhypusine + propane-1,3-diamine.
                                                                                         ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                         Gaps
                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COFACTOR: NAD (BY SIMILARITY)
-!- PATHWAY: Hypusine biosynthesis; first step.
-!- SIMILARITY: BELONGS TO THE DEOXYHYPUSINE SYNTHASE FAMILY.
dhys; 1.
s; Transferase; NAD; Complete proteome.
a1997 MW; 3DE853F38029EC55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probom; Prof. 13: 1.
TIGRROMS; TIGRO0321; dhys; 1.
Hypusine biosynthesis; Transferase; NAD; Complete proteome.
SEQUENCE 351 AA; 399781 WW; 7F7B306337FED7CD CRC64;
                                                          Score 43; DB 1; Length 335;
Pred. No. 3.5;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 351;
                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable deoxyhypusine synthase (EC 2.5.1.46) (DHS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 1;
Pred. No. 5.4;
                                                                                                                                                                                                                    351 AA.
                                                                                                                                                                                                                                                                                                                                                 Methanocaldococcaceae; Methanocaldococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U67525; AAB98813.1; ALT_INIT.
HSSP; P49366; 1DHS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002773; DS. * InterPro; IPR001230; Prenyl_site.
  TIGRFAMS, TIGR00321; dhys; 1.
Hypusine biosynthesis; Transfer
SEQUENCE 335 AA; 37997 MW;
                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
30-MAY-2000 (Rel. 39, Last seq
15-JUN-2002 (Rel. 41, Last anno
                                                            81.1%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.2%;
75.0%;
                                                                         Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                     Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01916; DS; 1.
                                                                                                                                1 EGPWLEEEE 9
                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                   OR MJ0814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR; MJ0814;
                                                                                                                                                                                                                 DHYS_METJA
                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 9
                                                                                                                                                                                                     DHYS_METJA
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Local Similarity

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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InterPro: IPR001909; XRAB.

InterPro: IPR000822; Znf_C2H2.

Pfam; PF010096; zf-C2H2; 11.

Pfam; PF010096; zf-C2H2; 11.

PROSITE; PS50805; KRAB; 1.

PROSITE; PS50805; ZINC_FINGER_C2H2_1; 11.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 11.

Transcription regulation; Zinc-finger; Metal-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                               genes, ZIM3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Pred. No. 7.3;
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                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Zinc finger imprinted 3.
                                                                                                                    472 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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C2H2-TYPE.
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C2H2-TYPE.
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C2H2-TYPE.
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tive 0;
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                                                                                                                    STANDARD;
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189
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DOMAIN 8
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1223
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361
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nes 7; Conserv
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                               35 EGPWLEDD 42
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                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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1 EGPWLEEE
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67 PWLEEEE

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"Chinchilla 'big' and 'little' gastrins.";
Blochem. Blophys. Res. Commun. 143:7-14(1987).
-!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chinchilla brevicaudata (Chinchilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Chinchillidae;
                                                                                                    Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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                                                                                                                                                                                                                                                                                                                                                     Hormone; Cleavage on pair of basic residues; Amidation PEPTIDE 1 33 GASTRIN (GASTRIN 33). PEPTIDE 18 33 GASTRIN GASTRIN 33). MOD_RES 18 18 PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       B37C251CD40EB30C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1989 (Rel: 10, Created)
01-MAR-1989 (Rel: 10, Last sequence update)
15-JUN-2002 (Rel: 41, Last annotation update)
                                            01-JAN-1988 (Rel. 06, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                       33 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40;
Pred. No.
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                        PRT;
                                                                                                                                                              SEQUENCE.
MEDLINE-86309993; PubMed-3747718;
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                                                                                                                                                                                                                                                                                                       PIR; A26089; GMGPB.
InterPro: IPR001651; Gastrin.
Pfam: PF00918; Gastrin: 1.
PROSITE: PS00259; GASTRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.5%;
75.0%;
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3757 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD; ,
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Best Local Similarity 75.v.
6. Conservative
                       STANDARD;
                                                                                                                                                                                                                                                                       and intestine.
                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
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NCBI_TaxID=10152;
                                                                                                                                         NCBI_TaxID=10141
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18 QGPWAEEE 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Big gastrin.
GAS.
                                                                              Big gastrin.
GAS.
                      GAST_CAVPO
P06885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAST_CHIBR
P10034;
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MOD_RES
MOD_RES
SEQUENCE
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GAST_CHIBR
RESULT 14
GAST_CAVPO
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and increases blood circulation and water secretion in the stomach and intestine.
                                                                                                                                                                                                                             Gaps
                                                                      InterPro; IPRO0151; Gastrin.
Pfam; PF00918; Gastrin: 1.
PROSITE; PS00259; GASTRIN: 1.
HOTMON: Cleavage on pair of basic residues; Amidation; Sulfation.
PEPTIDE 3 BIG GASTRIN (GASTRIN 33).
                                                                                                                                                                                                                            ;
                        -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
PIR; A29541; A29541.
PIR; B29541; B29541.
                                                                                                                                                                                                      Length 33;
                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID. SULFATION.
                                                                                                                                                                                                                          Indels
                                                                                                                      BIG GASTRIN (GASTRIN 33)
GASTRIN.
                                                                                                                                                                   AMIDATION.
6F11F5CDC50FAA2D CRC64;
                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                            Mismatches .
                                                                                                                                                                                                                                                                                                          Search completed: February 5, 2003, 09:48:17 Job time : 7.42857 secs
                                                                                                                                                                                                     Score 40;
Pred. No. 1
                                                                                                                                                                                                     75.5%;
75.0%;
                                                                                                                                                                              3715 MW;
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18
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QGPWAEEE 25
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PEPTIDE
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Best Local
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arabidopsis arabidopsis peanut stun

09spg8 023618 0

Q8zt18 pyrobaculum Q31205 mus musculu Q8w0d0 oryza sativ

QUOCO OTTA SALIV QBWLM9 mus musculu QBWLM9 mus musculu Q31615 mus musculu Q31206 mus musculu Q31206 nus musculu Q47v1 oryza sativ Q847s1 drosophila Q9vnu9 drosophila Q8v4f7 arabidopsis Q8v4f7 arabidopsis Q6q4 homo sapien Q8s16 zea mays (m Q8s16 zea mays (m

095PG8 023618 085018 0802118 08020 098718 031208 031208 031208 031206 097301 087351 087351 087351 09604 09604 09604 09604 09604 09604 09604 09604 09604 09604 09604 09604 09604 09604 09604

Offev3 oryza sativ O94ct3 oryza sativ O50069 arabidopsis O9fn86 arabidopsis O8zmf0 salmonella 091x82 arabidopsis O94ig1 arabis gemm P93391 nicotiana t O9x5f7 zymomonas m

Q91fel arabidopsis

ALIGNMENTS

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5, 2003; 09:45:51 ; Search time 21 Seconds (without alignments) 88.306 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                           parameters:
                                                                                                                                                                                                                                                                       671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            - protein search, using sw model
                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fung1:*
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sp_human:*
sp_invertebrate:*
sp_mhc:*
sp_organelle:*
sp_phage:*
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sp_lant:*
sp_rodent:*
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sp_vivus:*
sp_vivus:*
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                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 2000000000
                                                                                                                                                      US-09-700-329-1
53
1 EGPWLEEEE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPTREMBL_21:*
                                                                                           February
                                                                                                                                                         Title:
Perfect score:
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Maximum DB s
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                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

SUMMARIES

	Description	O9scpl arabidopsis		Q8x4r9 escherichia	Q94if9 arabidopsis	094if8 arabidopsis	Q94if6 arabidopsis	Q93vz0 arabidopsis		Q39028 arabidopsis	_	Q94jn5 gossyptum h	_	-	Q9fjp2 arabidopsis	-	-
	an 	Q9SCP1	088415	Q8X4R9	Q94IF9	Q94 IF8	Q94IF6	03VEQ	Q93V46	039028	049020	Q94JN5	Q94JN4	P81394	Q9FJP2	Q9CQD5	Q8VE83
	DB :	10	10	16	10	10	10	10	10	10	10	10	10	10	10	11	11
:	Match Length DB	238	160	248	273	273	273	273	273	273	293	293	293	268	310	311	311
% Query	Match	84.9	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	75.5	75.5	75.5	75.5
	Score	45	41	41	41	41	41	41	41	41	41	41	41	40	40	40	40
Result		1	2	m	4	S	9	7	89	6	10	11	12	13	14	15	16

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KESULT Q9SCP1 ID Q	P1 Q9SCP1 PRELIMINARY;	PRT;	238 AA.		
AC					
DI	(TrEMBLrel.				
E E	01-MAY-2000 (TremBirel. 13	13, Last seg	Last sequence update)		
DE	in.		oration update)		
N N	T4D2.130.				
SO	Arabidopsis thaliana (Mouse-ear cress).	se-ear cres	8).		
00	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Streptophy	ta; Embryophyta;	racheophyta;	
ဗ	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	yta; eudico	tyledons; core euc	licots; Rosida	e)
၁၀	eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Brassicace	ae; Arabidopsis.		
×o	NCBI_TaxID=3702;				
Z Z	[1]				
RP	SEQUENCE FROM N.A.				
RA	Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.,	, Dauner D.	, Sterr W., Holla		
RA	Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier	H.W., Lemc	ke K., Mayer K.F.	K., Quetier F.,	
RA	Salanoubat M.;				
RL	Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases	he EMBL/Gen	Bank/DDBJ databas	.88	
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	EU Arabidopsis sequencing project;	project;			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases	he EMBL/Gen	Bank/DDBJ databas	es.	
ပ္ပ	-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).	NUCLEAR (B	Y SIMILARITY).		
ပ္ပ	-! - SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS	2 MYB-LIKE	DOMAINS.		
DR	EMBL; AL132958; CAB64223.1;	1;			
DR	HSSP; P01103; 1POM.				
DR	InterPro; IPR001005; Myb_DNA_binding.	ONA_binding			
DR	Pfam; PF00249; myb_DNA-bir	oding; 2.			
DR	SMART; SM00395; SANT; 2.				
DR	PROSITE; PS50090; MYB_3; 2.	2.			
ΚW	DNA-binding; Nuclear protein.	ein.			
ŏs.	SEQUENCE 238 AA; 27996 MW;		B6DDCF70E22DE62E CRC64;		
Ouc	Query Match 84.9%; Rest Local Similarity 87.5%.		Score 45; DB 10; Length	າ 238;	
Ma	vat		g: '.3', atches 0; Indels	els 0; Gaps	S)
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28619 MW; DOF452DA2299E3D8 CRC64;

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EMBL; AP002562; BAB37034.1;
                         Complete proteome. SEQUENCE 248 AA;
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                                                                                                                                                                                                                                                                                                              Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
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MEDLINE-21074935, PubMed-11206551;
MEDLINE-21074935, PubMed-11206551;
MEDLINE-21074935, PubMed-11206551;
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Jiang C., Peterson T.;
Jiang C., Peterson T.;
Jiang C., Peterson T.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: AF470090: AAL90658-11. -.
TOWNER 160 AA, 17920 MW; IFCBA42C22AF1B89 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-f, hypothetical protein.
24066 OR ECS3611.
Escherichia coli 0157:H7.
                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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Pred. No. 24;
2; Mismatches 1;
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                                                                                                                                                                                                       Created)
                                                                                                                                                           PRT;
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Best Local Similarity 66./.
6; Conservative
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15 KGPWTEEED 23
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12 GPWLEEED 19
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GPWLEEEE 9
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Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                        Gaps
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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"Nucleotide polymorphism at the Atmyb2 locus of the wild plant
Arabidopsis thaliana.";
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Kamiya T., Kawabe A., Miyashita N.T.;
"Nucleotide polymorphism at the Atmyb2 locus of the wild plant
Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.4%; Score 41; DB 10; Length 273; 66.7%; Pred. No. 40; 1; Indels Live 2; Mismatches 1; Indels
  Length 248;
                                                           Indels
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PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
PROSITE; PS50034; MYB_2; UNKNOWN_1.
SEQUENCE 273 AA; 31416 MW; 737F99A3C287049E CRC64;
                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
MYB transcription factor Atmyb2.
                                                        1;
  77.4%; Score 41; DB 16; 66.7%; Pred. No. 37;
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                                                                                                                                                                                                                                                                                                    273 AA
                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
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InterPro; IPR001005; Myb_DNA_binding.
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                                                           Conservative
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nes 6; Conservative
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Query Match
Best Local Similarity
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234 QGPWLSKEE 242
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SEQUENCE FROM N.A.
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                                                                                                             1 EGPWLEEEE 9
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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C STRAIN-WS-0, KAS-1, AND OST-0;

A Kamiya T., Kawabe A., Miyashita N.T.;

A Kamiya T., Kawabe A., Miyashita N.T.;

"Nuclectide polymorphism at the Atmyb2 locus of the wild plant

T Arabidopsis thaliana.";

L Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL; AB052244; BAB62120.1;

R EMBL; AB052244; BAB62121.1;

R EMBL; AB052244; BAB62121.1;

R EMBL; AB052244; BAB62121.1;

R EMBL; AB05244; BAB62124.1;

R EMBL; AB05244; BAB62124.1;

R FOOTEP: IPR001005; Wyb_DNA_binding.

R PROSITE; PS00037; MYB_1; UNKNOWN_1.

R PROSITE; PS00037; MYB_1; UNKNOWN_1.

R PROSITE; PS000934; MYB_2; UNKNOWN_1.
                                              SEQUENCE FROM N.A.
STRAIN-VARIOUS STRAINS;
Kamiya T., Kawabe A., Miyashita N.T.;
Nucleotide polymorphism at the Atmyb2 locus of the wild plant
Arabidopsis thaliams..;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB052250; BAB62130.1; -.
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001395; Aldo/ket_red.
InterPro; IPR001395; Aldo/ket_red.
InterPro; IPR001005; Myb_DNA_binding.
Pfam; PF00249; myb_DNA-binding; 2.
PROSITE; PS00063; ALDOKEFO_REDUCTASE_3; UNKNOWN_1.
PROSITE; PS000334; MYB_1; UNKNOWN_1.
PROSITE; PS000334; MYB_2; UNKNOWN_1.
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EMBL, AB052232, BAB62112.1;
EMBL, AB052233, BAB62113.1;
EMBL, AB052236, BAB62116.1;
EMBL, AB052240, BAB62117.1;
EMBL, AB052240, BAB62120.1;
EMBL, AB052242, BAB62123.1;
EMBL, AB052242, BAB62123.1;
EMBL, AB052244;
EMBL, AB052241;
EMBL, AB052
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Best Local Similarity 66.7%;
Cahas 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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22 KGPWTEEED 30
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    NCBI_TaxID=3702;
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01-DEC-2001
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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T. Arabidopsis thaliana.";

T. Arabidopsis thaliana.";

T. Arabidopsis thaliana.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

R. EMBL, AB05239; BAB62119.1;

R. InterPro: IPR001305; Aldo/ket_red.

R. InterPro: IPR001005; Myb_DNA_binding.

R. Pfan: PF00249; myb_DNA_binding. 2.

R. PROSITE; PS000037; MYB_1: UNKNOWN_1.

R. PROSITE; PS00034; MYB_2: UNKNOWN_1.

R. PROSITE; PS00090; MYB_3: UNKNOWN_1.

R. PROSITE; PS00090; MYB_3: UNKNOWN_1.

R. PROSITE; PS00090; MYB_3: UNKNOWN_1.
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(DEC-2000) to the EMBL/GenBank/DDBJ databases.
             EMBL: ABOS 2255; BAB62115.1; -
InterPro: IPR001395; Aldo/ket_red.
InterPro: IPR001005; Myb_DNA_binding.
Pfam: PF00249; myb_DNA_binding.2.
PROSITE: PS000037; MYB_1; UNKNOWN_1.
PROSITE: PS00037; MYB_1; UNKNOWN_1.
PROSITE: PS00034; MYB_3; 2.
SEQUENCE 273 AA; 31429 MW; 52B5D2466790B9E6 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Pred. No. 40;
2; Mismatches 1
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66.78;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                             :||| |||:
22 KGPWTEEED 30
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22 KGPWTEEED 30
                                                                                                                                                                                                                                                                                                                                   1 EGPWLEEEE 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-IN-0;
  Submitted
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Q93VZ0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q94JN5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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DDT BDD READ BRAND BDD BDD BDD BBB BDB BBB BDB BBB BDB BBB BDB BBB BDB BBB BB BB BBB BB 
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Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
Spriggs T.A., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyladons; core eudicots; Rosidae;
Suromatophyta; Massicales; Brassicacee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-COLUMBIA;
MEDLINE-94146551; PubMed-8312738;
Urao T., Yamaguchi-Shinozaki K., Urao S., Shinozaki K.;
"An Arabidopsis myb homolog is induced by dehydration stress and its gene product binds to the conserved MYB recognition sequence.";
Plant Cell 5:1529-1539(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94BAE5F38C3854DF CRC64;
                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
ATWWIB2 (WYB transcription factor ATWYB2).
MYB2 OR T08113.3 OR ATWYB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
PROSITE; PS000037; MYB_1; UNKNOWN_1.
PROSITE; PS00034; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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66.7%; Pred. No. 40;
:ive 2; Mismatches 1
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                                                                                                                                                                                                                                     273 AA.
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                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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SEQUENCE 273 AA; 31448 MW;
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Best Local Similarity 60.,
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                                                                                                                                                                                                                                        PRELIMINARY;
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TRANSFAC; T02536; -
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                                                                 :||| |||:
22 KGPWTEEED 30
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                               1 EGPWLEEEE 9
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                                                                                                                                                                       RESULT 9
Q39028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gossypium hirsutum (Upland cotton).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                              STRAIN=CV. ACALA SJ-2; TISSUE=OVULE;
Loguercio L.L., Zhang J., Wilkins T.A.;
Structure and expression of six classes of myb-domain genes in allotetraploid cotton (Gossypium hirsutum L.).";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL; AF034133; AAC04719.1; -.
HSSP; P06876; 1MSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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STRAIN-CV. LANDRACE 'PALMERI';
STRAIN-CV. CADDIM W., Haselkorn T., Osborne C., Wendel J.F.;
"PCR-mediated recombination in a polyploid plant.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF377316; AAR57698 1; -
InterPro; IPR01005; Myb_DNA_binding.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
PROSITE; PS00334; MYB_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.4%; Score 41; DB 10; Length 293; 66.7%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 293;
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SEQUENCE 293 AA; 33746 MW; 06901890BD174772 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Myb-like transcription factor Myb 5.
                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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66.7%; Pred. No. 43;
tive 2; Mismatches 1
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NCBI_TaxID=3635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro: IPR001005; Myb_DNA_binding.
Pfam: PF00249; myb_DNA-binding; 2.
SMART; SM00395; SAMT; 2.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
PROSITE; PS00034; MYB_2; 1.
PROSITE: PS50090; MYB_3; 2.
                                                                              MYB-like DNA-binding domain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                    Gossypium hirsutum (Upland cotton).
01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
6, Conserve
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SEQUENCE FROM N.A.
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22 KGPWTEEED 30
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23 KGPWTEEED 31
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MYB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 310 AA; 35136 MW;
                                      31110 MW;
                                                                        75.5%;
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Best Local Similarity 66./*,
Best Local Similarity 66./*,
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
61
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                                      268 AA;
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                                                                                                 Local Similarity
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|5 GPWTEEED 22
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                                                                                                                                                       2 GPWLEEEE 9
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o
                  DNA_BIND
SEQUENCE
DNA_BIND
                                                                          Query Match
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                                                                                                                                                                                                                                                    RESULT 14
Q9FJP2
                                                                                                                   Matches
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0
                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PECTAIN 1:522; TISSUE-FLOWER BUDS; MEDLINE=93005689; PubMed=1840903; MEDLINE=93005689; PubMed=1840903; Jackson D., Culianez-Macia F., Prescott A.G., Roberts K., Martin C.; Expression patterns of myb penes from Antirrhinum flowers."; Plant Cell 3:115-125(1991). Plant Cell 8:115-125(1991). - I-FUNCTION: MAY BE A TRANSCRIPTIONAL ACTIVATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antirrhinum majus (Garden snapdragon).
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
                                                                                                                                                                                                                                                                                     TRANSFAC: T02927: ...
TRANSFAC: T02927: ...
InterPro: IPR001005; Myb_DNA_binding.
Pfam: PF00249: myb_DnA-binding; 2.
SMART: SM00395; SANTP: 2.
PROSITE: PS00037: MYB_1: UNKNOWN_1.
PROSITE: PS00034: WYB_1: 1.
PROSITE: PS00090: WYB_3: 2.
Nuclear protein: DNA-binding; Repeat; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 77.48; Score 41; DB 10; Length 293; Best Local Similarity 66.78; Pred. No. 43; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND MATURE FLOWER.
-!- SIMILARITY: BELONGS TO THE MYB FAMILY OF PROTEINS.
PIR; JQ061; JQ0961.
HSSP; Q03237; LA5J.
                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Myb-like transcription factor Myb 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                          PRT;
                                                                                                                                                                                          Gossypium hirsutum (Upland cotton)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2002 (TrEMBLrel. 20, MYB-related protein 315.
                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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23 KGPWTEEED 31
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                                                                        Q94JN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P81394
                                  RESULT 12
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                                                    Q94JN4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription factor-like protein.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned Pl and TaC clones.";

DNA Res. 5.203-216(1988).

-! SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-! STATLARITY: CONTAINS 2 MYB-LIKE DOMAINS.

EMBL; AB013395; BAB11659.1;

-InterPro; IPR001005; Myb_DNA_binding.
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                                                                            Length 268;
                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9070DD86A4C2AF9D CRC64;
                       886C04A4F45D26D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                            Score 40; DB 10;
Pred. No. 58;
1; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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SMART; SM00395; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98403884; PubMed=9734815;
MYB
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MEDLINE-21085660; PubMed-11217851;

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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arawa K., Izawa M., Mishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,
RA Fielschmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
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RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Boffelli B., Boffelli B., Barsh G.,
RA Braka J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brake J., Morfoloni L., Mashima J., Mombaerts P.,
RA Lyons P., Marchionni L., Mashima J., Mombaerts P.,
Rasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Stoch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Stoch K.-F.,
RA Bayashizaki Y.;
RHA Hayashizaki Y.;
Rhuctional annotation of a full-length mouse cDNA collection.";
RMI, AKUIS65; BAB28730.1;
REMBL, AKUIS133; BAB28730.1;
REMBL, AKUIS165; BAB28730.1;
REMBL, AKUIS165; BAB28730.1;
REMBL, AKUIS165; BAB28730.1;
REMBL, AKUIS165; BAB28830.1;
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Best Local Similarity 66.7
Matches 6; Conservative
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Search completed: February 5, 2003, 09:49:14 Job time: 22 secs

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EARLIER FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
8
1
8
10
27
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MOD_RES
 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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                                            ; Search time 117 Seconds
(without alignments)
49.595 Million cell updates/sec
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Sequence 1, 1
Sequence 7, 1
Sequence 1, 1
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                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/paa/US60_COMB.pep:
      GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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PCT-US99-10751-1
US-08-798-423-7
US-09-700-329-1
US-09-700-378-7
US-09-700-402-1
                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                      4569144 segs, 644733110 residues
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                                             5, 2003, 09:48:26
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Maximum Match 100%
Listing first 45 summaries
                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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53
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Match Length
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Sequence 6, Applisequence 60, Applisequence 422, Applisequence 75, Applisequence 75, Applisequence 75, Applisequence 76, Applisequence 76, Applisequence 10, Applisequence 11, Applisequence 69, Applisequence 69, Applisequence 69, Applisequence 69, Applisequence 69, Applisequence 106, Applisequence 106, Applisequence 106, Applisequence 106, Applisequence 100, Applisequence 99, Applisequence 99, Applisequence 97, Applisequence 77, Applisequence 1756, Applisequence 2, Applisequence 2,
                                                                                Sequence 10, Appl
       Sequence 1, i
Sequence 10,
                                                                                                                                                                                                                                                                                           PCT-US94-04832A-75
US-08-488-320A-75
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US-08-68-34-546-10
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US-08-488-320A-95
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US-09-506-854-10
US-10-016-306-10
US-08-798-423-6
PCT-USO2-22821-60
US-08-929-095-2
US-09-657-276-422
US-10-197-954-60
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US-60-195-053-1756
US-60-163-123-1073
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APPLICANT: Geras, Philip C.
APPLICANT: Grimes, Stephen
APPLICANT: Grimes, Stephen
APPLICANT: Michaeli, Dov
APPLICANT: Michaeli, Dov
APPLICANT: Aphton Corporation
TITLE OF INVENTION: Disease
FILE REFERENCE: ACGIPCT
CURRENT APPLICATION NUMBER: PCT/US99/10734
EMRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: 60/085,610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: Description of Unknown Organism:
OTHER INFORMATION: synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: pyroglutamic acid
Sequence 7, Application PC/TUS9910734 GENERAL INFORMATION:
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Result

Gaps

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Indels

; 0

Mismatches

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9; Conservative
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US-09-700-329-1
        Matches
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GENERAL INFORMATION:
APPLICANT: APHTON CORPORATION
TITLE OF INVENTION: Prevention and Treatment of Hypergastrinemia
FILE REPERBNCE: 1102865-0035
CURRENT APPLICATION NUMBER: PCT/US99/10751
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: US|60/065,714
BARLIER FILING DATE: 1999-05-15
NUMBER OF SEO ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methods for the Treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 9;
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                                           Length D
                                    100.0%; Score 53; DB 1; 1
100.0%; Pred. No. 4.2e+06;
iive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53; DB 11;
Pred. No. 4.2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gevas, Philip C.
APPLICANT: Gevas, Philip C.
APPLICANT: Gevas, Philip C.
APPLICANT: Gevas, Stephen L.
APPLICANT: Gines, Stephen C.
APPLICANT: Michaell, Dov
APPLICANT: Matson, Susan A.
TITLE OF INVENTION: Immunological Methods for TITLE OF INVENTION: Gastrointestinal Cancer FILE REFERENCE: 110286-0031
CURRENT APPLICATION NUMBER: 60/011,411
PRIOR APPLICATION NUMBER: 60/011,411
PRIOR APPLICATION NUMBER: 60/011,411
PRIOR APPLICATION NUMBER: 60/011,411
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
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. OTHER INFORMATION: Pyroglutamic acid residue
US-08-798-423-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)
CTHER INFORMATION: pyroglutamic acid
PCT-US99-10751-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08798423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
100.0%;
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                Ouery Match
Best Local Similarity الان.
و، Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                         1 EGPWLEEEE 9
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                                                                                                                  EGPWLEEEE
                                                                                                                                                                                                                   RESULT 2
PCT-US99-10751-1
PCT-US99-10734-7
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US-08-798-423-7
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LENGTH: 9
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LENGTH: 9
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APPLICANT: Gevas, Philip
APPLICANT: Stephen, Grimes
APPLICANT: Karr Stephen
APPLICANT: Michaell, Dov
TITLE OF INVENTION: Method for the Treatment of Gastroesophageal Reflux Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                 APPLICANT: Gevas, Philip
APPLICANT: Grimes, Stephen
APPLICANT: Karr, Stephen
APPLICANT: Karr, Stephen
APPLICANT: Matson, Susan
TITLE OF INVENTION: Prevention and Treatment of Hypergastrinemia
CURRENT APPLICATION UNBER: US/09/700,329
CURRENT APPLICATION DATE: 2001-02-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 2001-02-08
PRIOR APPLICATION NUMBER: PCT/US99/10751
PRIOR FILING DATE: 1999-05-14
PRIOR FLING DATE: 1998-05-15
PRIOR FLING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 1
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/700,378
CURRENT FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: PCT/US99/10734
PRIOR FILING DATE: 1999-05-14
PRIOR PLING DATE: 1999-05-15
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)..(1)
COTHER INFORMATION: pyroglutamic acid
US-09-700-329-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : LOCATION: (1)..(1); OTHER INFORMATION: pyroglutamic acid US-09-700-378-7
                                                                                                                                            Sequence 1, Application US/09700329 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-09-700-378-7
; Sequence 7, Application US/09700378
; GENERAL INFORMATION:
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ORGANISM: human gastrin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 9; Conservative
EGPWLEEEE 9
                       1 EGPWLEEEE 9
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ORGANISM: human
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Gaps
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Sequence 10, Application US/10016306
GENERAL INFORMATION:
APPLICANT: Cheng, J111
Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
PHOSPHATASE, PTP LAMBDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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ADDRESSEE: FLEHR HOHBACH TEST ALBRITTON & HERBERT LLP
                                                                                                                                                                                       APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR HOHBACH TEST ALBRITTON & HERBERT LLP
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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100.0%; Pred. No. 0.37;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 39,054
REFERENCE/DOCKET NUMBER: A-63478-4/DAV
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 781-1989
FELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/991,953
FILING DATE: 16-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,971
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Vance, Dolly A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/506,854 FILING DATE: 17-FEB-2000
                                                                                                                          US-09-506-854-10
; Sequence 10, Application US/09506854
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 STREET: 4 Embarcauero
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 amino acids
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Best Local Similarity 100.

Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
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                        EGPWLEEEE
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: APHTON CORPORATION
TITLE APHTON CORPOINATION
FILE REFERENCE: 1102865-0034
CURRENT APPLICATION NUMBER: US/09/700,402
CURRENT APPLICATION NUMBER: US/09/700,402
CURRENT FILING DATE: 1998-05-15
NUMBER OF SED ID NOS: 2
SOFTWARE: PALCHIN Ver. 2.0
SEQ ID NO 1
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1. Application US/08798423

GENERAL INFORMATION:
APPLICANT: Gevas, Philip C.
APPLICANT: Garnes, Stephen L.
APPLICANT: Matches, Stephen C.
APPLICANT: Michaeli, Dov
APPLICANT: Watchon, Sucan A.
TITLE OF INVENTION: Immunological Methods for the Treatment of
TITLE OF INVENTION: Gastrointestinal Cancer
FIRE REFERENCE: 1102865-0031
CURRENT APPLICATION NUMBER: 60/011,411
PRIOR APPLICATION NUMBER: 60/011,411
PRIOR FILING DATE: 1997-02-07
PRIOR FILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
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    Length 9;
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                                           Indels
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100.0%; Score 53; DB 21;
100.0%; Pred. No. 4.2e+06;
iive 0; Mismatches 0;
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100.0%; Pred. No. 4.2e+06;
Live 0; Mismatches 0;
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; OTHER INFORMATION: Pyroglutamic acid residue
US-08-798-423-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MOD_RES
LOCATION: (1)
COTHER INFORMATION: pyroglutamic acid
US-09-700-402-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: human or synthetic peptide
                   Best_Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
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ORGANISM: Homo sapiens
                                                                                1 EGPWLEEEE 9
                                                                                                        1 EGPWLEEEE 9
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                                                                                                                                                                                                             US-09-700-402-1
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LENGTH: 12
  Query Match
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Sequence 2. Application US/08929095
GENERAL INFORMATION:
APPLICAMY: Sportsman, Richard
APPLICAMY: Sportsman, Richard
APPLICAMY: Sportsman, Nicholas
APPLICAMY: Lawrence
APPLICAMY: Lawrence
APPLICAMY: Lee, Sandra
APPLICAMY: NITIAL
APPLICAMY: NITIAL
APPLICAMY: NITIAL
APPLICAMY: NITIAL
APPLICAMY: NITIAL
APPLICAMY: Lee, Sandra
APPLICAMY: Lee, Sand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: No Final Manageculicats, inc.
APPLICANT: Roister, Hubert
APPLICANT: Siddigi, Suhalb
APPLICANT: Siddigi, Suhalb
APPLICANT: Little, Daniel
TITLE OF INVENTION: Capture Compounds, Collections Thereof
TITLE OF INVENTION: Compositions
FILE REFERENCE: 24743-2306
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 60/306,019
PRIOR PAPLICATION NUMBER: 60/306,019
PRIOR PLING DATE: 2001-08-21
PRIOR PPLING DATE: 2001-08-21
PRIOR PPLING DATE: 2002-03-11
NUMBER OF SEQ ID NOS: 149
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 60
LENGTH: IT
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                                                                                                               100.0%; Score 53; DB 11; Length 16; 100.0%; Pred. No. 0.49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 53; DB 13; Length 17;
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                                                                                                                                                                                         Indels
                                                                                                                                                                                         ..
; OTHER INFORMATION: Pyroglutamic acid residue US-08-798-423-6
                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US02-22821-60; Sequence 60, Application PC/TUS0222821; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HK Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                               Query Match 100.

Best Local Similarity 100.

Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo Sapien
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GENERAL INFORMATION:
APPLICANT: Gevas, Philip C.
APPLICANT: Grimes, Stephen L.
APPLICANT: Michaell, Dov
APPLICANT: Watson, Susan A.
TITLE OF INVENTION: Immunological Methods for the Treatment of
TITLE OF INVENTION: Gastrointestinal Cancer
FILE REFERENCE: 1102865-0031
CURRENT APPLICATION NUMBER: US/08/798,423
CURRENT FILING DATE: 1997-02-07
PRIOR PELING DATE: 1997-02-08
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 6
LENGTH: 16
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                                                                                                                                 COMPUTER READABLE FORM:

MEDLUM TYPE: Eloppy#disk

COMPUTER: ISOPPy#disk

COMPUTER: ISOPPy#disk

COMPUTER: ISOPPy#disk

COMPUTER: ISOP Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/016,306

FILING DATE: 10-Dec-2001

CLASSIFCATION OF CURNOWN>

PRIOR APPLICATION NUMBER: US/09/506,854

FILING DATE: CUNROWN>

APPLICATION NUMBER: US 08/91,953

FILING DATE: 16-DEC-1997

APPLICATION NUMBER: US 08/652,971

FILING DATE: 14-MAY-1996

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 53; DB 24; Length 12; Best Local Similarity 100.0%; Pred. No. 0.37; Matches 9; Conservative 0; Mismatches 0; Indels
       STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Vance, DOLLY A.
REGISTRATION NUMBER: 39,054
REFERENCE/DOCKET NUMBER: 3-63478-4/DAV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELERX: (415) 389-3249
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-10-016-306-10
                                        CITY: San Francisco
STATE: California
COUNTRY: United Sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EGPWLEEEE 9
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LOCATION: (1)
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; ORGANISM: Homo Sapien
US-10-197-954-60
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PCT-US94-04832A-75
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                                                                                                                                                                                                                                                                                            APPLICANT: Bridon, Dominique
APPLICANT: Bridon, Dominique
APPLICANT: Bridon, Dominique
APPLICANT: Bridon, Dominique
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darten
APPLICANT: Thibaudeau, Karen
TITLE OF INVENTION: PROPECTION OF ENDOGENOUS THERAPBUTIC PEPTIDES FROM
TITLE OF INVENTION: COMPÓNENTS
TITLE OF INVENTION: DAMBER: US/09/657,276
CURRENT FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR PELING DATE: 1999-05-10
PRIOR PELING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 422
LENTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 60, Application US/10197954;
GENERAL INFORMATION:
APPLICANT: K'ster, tubert
APPLICANT: Siddiqi, Suhaib
APPLICANT: Siddiqi, Suhaib
APPLICANT: Siddiqi, Suhaib
APPLICANT: Little, Daniel
TITLE OF INVENTION: Capture Compounds, Collections Thereof
TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
TITLE OF INVENTION: Compositions
FILE REFERENCE: 24743-2305
CURRENT APPLICATION NUMBER: 80/306
PRIOR PLILING DATE: 2002-07-16
PRIOR PELICATION NUMBER: 60/314,123
PRIOR PLILING DATE: 2001-08-21
PRIOR PLILING DATE: 2001-08-21
PRIOR PLILING DATE: 2003-03-11
NUMBER OF SEQ ID NOS: 149
SOFTWARE: FastSEQ for Windows Version 4.0
                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide US-09-657-276-422
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                        0; Indels
Pred. No. 0.52;
                        Mismatches
                                                                                                                                                                                                                                    Sequence 422, Application US/09657276
GENERAL INFORMATION:
APPLICANT: Conjuchem, Inc.
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  100.0%;
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Best Local Similarity 100.
Matches 9; Conservative
Best Local Similarity 100.
Matches 9; Conservative
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APPLICANT: Ladd, Anna
APPLICANT: Ladd, Anna
APPLICANT: Ladd, Chang Yi
APPLICANT: Camb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE:
STREET: 400 Garden City Plaza
CITY: Garden City
CITY: Garden City
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04832A
100.0%; Score 53; DB 25;
100.0%; Pred. No. 0.52;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB
Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: PCT/US94/04832A
13-APR-1994
                                                                                                                                                                                                      Sequence 75, Application PC/TUS9404832A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: (516)742-4343
TELEFAX: (516)742-4366
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.3%;
88.9%;
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 88.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 amino acids
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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PCT-US94-04832A-75
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Sequence 140, Application US/10302267
GENERAL INFORMATION:
APPLICANT: Keddie, James
APPLICANT: Fromm, Michael
APPLICANT: Heard, Jacqueline
APPLICANT: Riechmann, Jose Luis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adam, Luc
Broun, Pierre
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EGPWLEEEE
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US-10-302-267-140
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APPLICANT:
APPLICANT:
APPLICANT:
SEQ ID NO 7
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Sequence 114, App
Sequence 114, App
Sequence 114, App
Sequence 1980, Ap
Sequence 24, Appl
Sequence 1, Appl
Sequence 86993, A
Sequence 86993, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 206, App
Sequence 206, App
Sequence 86996, A
Sequence 86996, A
Sequence 86994, A
Sequence 86994, A
Sequence 18, Appl
Sequence 18, Appl
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Sequence 140, App
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 56304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                           2003, 09:48:01; Search time 14.5714 Seconds (without alignments) 50.530 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
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Sequence 5
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1. /cgn2_6/ptodata/1/paa/USO6_NEW_COMB.pep:*

2. /cgn2_6/ptodata/1/paa/USO6_NEW_COMB.pep:*

3. /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

4. /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

5. /cgn2_6/ptodata/1/paa/USO_NEW_COMB.pep:*

5. /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

7. /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

7. /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*
               GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 10-202-267-140
US 110-278-138
US-110-278-536-114
US-110-278-536A-114
US-110-218-140-1980
US-110-218-140-1980
US-110-218-140-1980
US-10-274-676-86993
US-10-278-536-206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-724-676-86995
US-09-724-676A-86995
US-09-724-676-51589
US-09-724-676-51590
US-09-724-676-51591
                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-314-057-7
                                                                                                                                                                                                                                                                                                412725 seqs, 81809943 residues
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                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                  length: 0
length: 2000000000
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53
1 EGPWLEEEE 9
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Match Length DB
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                                                                                                               February
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Maximum DB seq
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Sequence 7, Application US/10314057

GENERAL INFORMATION:

APPLICANT: Geves, Philip

APPLICANT: Stephen, Grimes

APPLICANT: Stephen, Grimes

APPLICANT: Michaell, Dov

ITILE OF INVENTION: Method for the Treatment of Gastroesophageal Reflux Disease

FILE REFERENCE: ACGIUSA

CURRENT FILING DATE: 2002-12-06

PRIOR APPLICATION NUMBER: US/10/314,057

CURRENT FILING DATE: 2000-11-14

PRIOR PRILING DATE: 1999-05-14

PRIOR FILING DATE: 1999-05-14

PRIOR PLING DATE: 1999-05-14

PRIOR FILING DATE: 1998-05-15

NUMBER OF SEO ID NOS: 8

SOFTWARE: PatentIn version 3.0
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51592,
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51598,
51599,
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                  US-09-724-676-51594
US-09-724-676-51594
US-09-724-676-51596
US-09-724-676-51596
US-09-724-676-51598
US-09-724-676-51598
US-09-724-676-51599
US-09-724-676-51599
US-09-724-676-51599
US-09-724-676A-51591
US-09-724-676A-51593
US-09-724-676A-51593
US-09-724-676A-51593
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US-09-724-676A-51595
US-09-724-676A-51595
US-09-724-676A-51595
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US-09-724-676A-51595
US-09-724-676A-51595
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US-09-724-676A-51595
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100.0%; Pred. No. 3.4e+05;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)..(1); OTHER INFORMATION: pyroglutamic acid US-10-314-057-7
                                                  Query Match
Best Local Similarity 100.
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Broun, Pierre
TITLE OF INVENTION: STRESS-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-011
CURRENT APPLICATION NUMBER: US/10/278,536
CURRENT FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 114
LENGTH: 349
                                                                                                                                                                                                          Score 40; DB 6;
Pred. No. 38;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 114, Application US/10278536A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 114, Application US/10278536 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reuber, Lynne
Riechmann, Jose-Luis
Yu, Guo-Liang
Keddie, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Riechmann, Jose-Luis
                                                                                          TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                          75.5%;
PRIOR FILING DATE: 1999-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Samaha, Raymond
APPLICANT: Heard, Jacqueline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keddie, James
Ratcliffe, Oliver
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Jiang, Cai-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jiang, Cai-zhong
Pineda, Omaira
Reuber, Lynne
                 NUMBER OF SEQ ID NOS: 177
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                      Ouery Match
Best Local Similarity 60.,
اتاء 6; Conservative
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Adam, Luc
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guo-Liang
                                                                                                                             ; FEATURE:
; OTHER INFORMATION: G220
US-10-278-173-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: G220
US-10-278-536-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yu, Guo-
Keddie,
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15 KGPWLPEED 23
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15 KGPWLPEED 23
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                                 SOFTWARE: Pate
SEQ ID NO 138
LENGTH: 349
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APPLICANT:
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TITLE OF INVENTION: POLYNUCLEOTIDES FOR ROOT TRAIT ALTERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6; Length 238;
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                                                                                                                                           TITLE OF INVENTION: PLANT GENE SEQUENCES II FILE REFERENCE: MBI-0007
CURRENT APPLICATION UMBER: US/10/302,267
CURRENT FILING DATE: 2002-11-22
                                                                                                                                                                                                CURREWY FILLING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US/09/506,720
PRIOR PLILING DATE: 2000-02-17
PRIOR PELICATION NUMBER: US/09/506,720
PRIOR PELICATION NUMBER: 60/120,880
PRIOR FILLING DATE: 1999-02-18
PRIOR FILLING DATE: 1999-03-11
PRIOR PLICATION NUMBER: 60/124,278
PRIOR APPLICATION NUMBER: 60/124,278
PRIOR PLICATION NUMBER: 60/129,450
PRIOR PLICATION NUMBER: 60/129,450
PRIOR FILLING DATE: 1999-04-15
PRIOR FILLING DATE: 1999-07-15
PRIOR FILLING DATE: 1999-07-15
PRIOR PELICATION NUMBER: 60/161,143
PRIOR FILLING DATE: 1999-10-22
PRIOR FILLING DATE: 1999-11-01
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CURRENT APPLICATION NUMBER: US/10/278,173
CURRENT FILING DATE: 2002-10-21
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Pred. No.
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PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 60/125,814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jiang, Cai-Zhong
APPLICANT: Broun, Pierre
Broun, Jose-Luis
APPLICANT: Pineda, Omaira
APPLICANT: Zhang, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yu, Guo-Liang
Pilgrim, Marsha
Keddie, James
Heard, Jacqueline
Reuber, Lynne
Ratcliffe, Oliver
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                                                                        Jiang, Cai-Zhong
                                                                                                                             Creelman, Robert
                                                                                                            Pilgrim, Marsha
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Best Local Similarity 87.5
Matches 7; Conservative
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US-10-302-267-140
                                                 ľu, Ğuo-Liang
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                                                                                        Samaha,
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Gevas, Philip
APPLICANT: Stephen, Grimes
APPLICANT: Stephen
APPLICANT: Stephen
APPLICANT: Stephen
APPLICANT: Stephen
APPLICANT: Machaeli, Dow
TITLE OF INVENTION: Method for the Treatment of Gastroesophageal Reflux Disease
FILE REFERENCE: ACGIOSA
CURRENT APPLICATION NUMBER: US/10/314,057
CURRENT FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 12
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                             APPLICANT: FALLENDON, MAIGHER; TREBOULEY, Catherine M.;
APPLICANT: THORNTON, MAIGHER; TREBOULEY, VICKI S.;
APPLICANT: U, Yan; ISON, CTABJ H.;
APPLICANT: U, Yan; ISON, CTABJ H.;
APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
APPLICANT: MARCUS, Gregory A.; ZINGLER, Kutt A.;
APPLICANT: MARCUS, Gregory A.; ZINGLER, Kutt A.;
APPLICANT: RARKUMAR, Jayalaxni; WARREN, Bridget A.;
APPLICANT: RAMKUMAR, Jayalaxni; WARREN, BRIDGET, DON 10-08-31
PRIOR APPLICATION NUMBER: US 60/236,499
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/234,902
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/231,357
PRIOR APPLICATION NUMBER: US 60/232,634
PRIOR APPLICATION NUMBER: US 60/232,634
PRIOR APPLICATION NUMBER: US 60/231,357
PRIOR APPLICATION NUMBER: US 60/231,357
PRIOR APPLICATION NUMBER: US 60/231,357
PRIOR APPLICATION NUMBER: US 60/232,634
PRIOR APPLICATION NUMBER: US 60/232,834
                                              Catherine M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 6;
Pred. No. 2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7477484CD1
US-10-288-798-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-314-057-1; Sequence 1, Application US/10314057; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.6%;
85.7%;
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Best Local Similarity
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APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 1596-543 CON
CURRENT APPLICATION NUMBER: 02/10/218,140
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 60/127,738
PRIOR FILING DATE: 1999-04-05
SOFTWARE: CUTANALOR VESSION 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 349;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                     APPLICANT: APELCANT: APELCANT: APPLICANT: Broun, Pierre
APPLICANT: Broun, Pierre
TITLE OF INVENTION: STRESS-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-011
CURRENT APPLICATION NUMBER: US/10/278,536A
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 114
LENGTH: 39
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Sequence 24, Application US/10288798

GENERAL IRFORMATION:
APPLICANT: BANDMAN, Olga; NGUYEN, Danniel B;
APPLICANT: WALIA, Narinder K.; HARALIA, April J.A.;
APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
APPLICANT: GURURAJAN, Rajagopal; DING, Li;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4e+02;
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Pred. No. 38;
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Pred. No. 1.4e+02
1; Mismatches
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ORGANISM: Arabidopsis thaliana
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75.0%;
Ratcliffe, Oliver
Pilgrim, Marsha
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Best Local Similarity 66./*,
6; Conservative
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; OTHER INFORMATION: G220
US-10-278-536A-114
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US-10-218-140-1980
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Best Local Similarity
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15 KGPWLPEED 23
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171 ŒWAEEEK 178
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LENGTH: 929
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APPLICANT:
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Pred. No. 62;
                                                                                                                                DB 6; Length 12; 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 86993, Application US/09724676A; Sequence 86993, Application US/09724676A; GENERAL INFORMATION:
APPLICANT: Compugen LTD:
TITLE OF INVENTION: Variants of alternative splicing; FILE REFERENCE: 129181.4 Compugen; CURRENT APPLICATION NUMBER: US/09/724,676A; CURRENT FILING DATE: 2000-11-28; NUMBER OF SEQ ID NOS: 97222; SOFTWARE: Patentin version 3.2; SEQ ID NO 86993.1
                                                                                                                                                                                                                                                                                                               Sequence 86993, Application US/09724676; GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222; SOGTWARE: Patentin version 3.2
SEQ ID NO 86993
LENGTH: 173
                                                                                                                                     71.7%; Score 38; DB 100.0%; Pred. No. 3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                  NAME/KEY: MOD_RES
: LOCATION: (1)...(1)
: CTGRIEN INFORMATION: pyroglutamic acid
US-10-314-057-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-10-278-536-206
Sequence 206, Application US/10278536
; GENERAL INFORMATION:
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55.6%;
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                     Query Match 71.7
Best Local Similarity 100.
Matches 6; Conservative
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CORGANISM: Homo sapiens
US-09-724-676-86993
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87 KGPWTKEED 95
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87 KGPWTKEED 95
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US-09-724-676A-86993
   TYPE: PRT
ORGANISM: human
FEATURE:
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| EGPWLE 6
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Pred. No. 1.2e+02;
3; Mismatches 1; Indels
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55.6%; Pred. No. 1.2e+02;
tive 3; Mismatches 1; Indels
                                                                                               APPLICANT: Yu, Guo-Liang
APPLICANT: Keddie, James
APPLICANT: Ratcliffe, Oliver
APPLICANT: Pigrim, Marsha
APPLICANT: Adam, Luc
APPLICANT: Adam, Luc
TITLE OF INVENTION: STRESS-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MB1-01
CURRENT APPLICATION NUMBER: US/10/278,536
CURRENT APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 238
SOFTWARE: PATENTIN VET: 2.1
LENGTH: 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Adam, Luc
APPLICANT: Broun, Pierre
TITLE OF INVENTION: STRESS-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-011
CURRENT APPLICATION NUMBER: 2002-12-09
CURRENT FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 206, Application US/10278536A; GENERAL INFORMATION:
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Yu, Guo-Liang
Keddie, James
Ratcliffe, Oliver
Pilgrim, Marsha
Adam, Luc
                                                                                  Riechmann, Jose-Luis
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55.6%;
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APPLICANT: Heard, Jacqueline
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Pineda, Omaira
Heard, Jacqueline
Jiang, Cai-Zhong
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
                                        Pineda, Omaira
Reuber, Lynne
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; OTHER INFORMATION: G216
US-10-278-536-206
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US-10-278-536A-206
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50 KGPWLPEQD 58
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                                                                                                                                   Sequence 86996, Application US/09724676
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000;11-28
NUMBER OF SEQ ID NOS: 97222;
SOFTWARE: Patentin version[3.2]
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Sequence 86996, Application US/09724676A
Sequence 86996, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILIG DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 86996
LENGTH: 493
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILIKO DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 86994
: LENGTH: 538
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Matches 5; Conservative
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; ORGANISM: Homo sapiens
US-09-724-676-86996
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; ORGANISM: Homo sapiens
US-09-724-676A-86996
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US-09-724-676-86994
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50 KGPWLPEQD 58
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87 KGPWTKEED 95
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87 KGPWTKEED 95
1 EGPWLEEEE 9
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US-09-724-676-86996
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US-09-724-676-86994
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Query Match
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 EGPWLEEEE 9
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Db 87 KGPWTKEED 95
Search completed: February 5, 2003, 09:50:58
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February 5, 2003, 09:40:45; Search time 35.4286 Seconds (without alignments) 45.133 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     908470 segs, 133250620 residues
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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75
1 ELGPQGRPPPPC 12
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Perfect score:
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Maximum DB :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SIDS2/ggddata/geneseq_geneseq_rembl_AA1991_DAT: *
| SIDS2/gcgdata/geneseq_geneseq_embl_AA1991_DAT: *
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*

Human gastrin G34
Human gastrin G34
Human tetratriacon
Gastrin hapten. H
Novel human secret
Novel human secret
Human polypeptide
Human polypeptide
Antigenic peptide Antigenic peptide Description SUMMARIES AAY49307 AAR62738 AAU30337 AAU30339 AAO07572 AAO00748 AAY51306 AAY51313 AAR06335 Π 11 22 22 22 22 22 22 11 Query Match Length 100.0 100.0 100.0 100.0 74.7 73.3 73.3 66.7 66.7 Score Š

Human gastrin G17	Himan nolvoentide	au		GnRH immunomimic a	Gonadotropin relea		Human ORFX ORF2550	Propionibacterium	Herpesviral VP22 p	UL26 protease dele	e Huntingt	Drosophila melanog	protease		protease		protease su		protease				L UL26 qen	UL26 protease inse	٥	protease	Puntingt	Mouse huntingtin p	Novel human diagn	aastrin	an hepta	human	
AAY51310	AA000530	AAB38442	199	AAR78285	AAY58141	AAG66081	AAB42786	AAU48788	AAW69717	AAR28638	AAW26545	ABB59725	AAR28641	AAR28642	AAR28640	AAR28634	AAR28650	AAR28649	AAR28651	AAR28652	AAR28647	AAR28648	AAR71031	AAR28635	AAR28636	AAR28637	AAW36888	AAW44743		AAY51312	AAY49306	92	557
21	22	21	22	16	21	23	21	22	19	13	18	22	13	13	13	13	13	13	13	13	13	13	16	13	13	13	18	19	22	21	21	22	22
11	146	383	383	16	16	16	102	118	362	415	418	463	603	615	626	635	635	635	635	635	635	635	635	989	989	636	3119	급	674	12	12	119	134
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4 4	49	49	49	48	48	48	48	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	4	46.5	46		46	
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ALIGNMENTS

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Juman gastrin G34 derived immunogen hG34(6).
              AAY51313 standard; peptide; 12 AA.
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Matches 12; Conserv
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                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                 WO9959631-A1
                                                                                                                                                                                                                                                                              14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic; treatment; hypergastrinemia; gastrin G17; gastrin G34;
pernicious anemia; anti-ulceq; proton pump inhibitor; colorectal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel method for the treatment or preventing hypergastrinemia by administering to a patient a gastrin G17 and/or G34 peptide fragment linked by an amino acid spacer to an immunogenic carrier. The methods are used to treat hypergastrinemic patients, particularly those with pernicious anemia, those receiving treatment with anti-ulcer agents such as proton pump inhibitors (particularly comeprazole or lansoprazole) or H.2 receptor blocking agents or antagonists, or those having colorectal disorders or diseases. This sequence represents the human gastrin G34 peptide which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eating or preventing hypergastrinemia comprising administration of,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Antigenic fragments may be attached to an immunogenic carrier and used to raise Abs to a specific single form of Gastrin ie. G17 or G34. Peptide fragments capable of binding to these Abs are useful in neutralising anti-gastrin Abs in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 75; DB 21; Length 12; larity 100.0%; Pred. No. 0.00093; Conservative 0; Mismatches 0. Thank
                                                                                                          ; Score 75; DB 11; Length 12;
; Pred. No. 0.00093;
0; Mismatches 0; Indels
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                                                                                                           100.0%;
100.0%;
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                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 AA;
                                                                             12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09959631-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                             14-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gevas PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                Seguence
                                                                                                                                                                                                                                                                                                              AAY51306;
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Matches
                                                                                                                                                                                                                                                    RESULT 2
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RESULT 3

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Immunogenic; treatment; hypergastrinemia; gastrin G17; gastrin G34;
pernicious anemia; anti-ulcer; proton pump inhibitor; colorectal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel method for the treatment or preventing hypergastrinemia by administering to a patient a gastrin G17 and/or G34 peptide fragment linked by an amino acid spacer to an immunogenic carrier. The methods are used to treat hypergastrinemic patients, particularly those with pernicious anemia, those receiving treatment with anti-ulcer agents such as proton pump inhibitors (particularly omeprazole or lansoprazole) or H_2 receptor blocking agents or antagonists, or those having colorectal disorders or diseases. This sequence represents a human gastrin G34 derived immunogen which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gastroesophageal reflux disease; GERD; gastrin; anti-gastrin antibody; histamine H_2; proton pump inhibitor; acid output; stomach; therapy; esophagitis; immunogen; human; tetratriacontagastrin; G34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or preventing hypergastrinemia comprising administration of,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human tetratriacontagastrin (G34) immunogenic peptide 5.
                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 75; DB 21;
100.0%; Pred. No. 0.00093;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                    Michaeli D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 18; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY49307 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       Karr S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g. anti-gastrin antibodies
                                                                                                                                                                                                                                                                                                         98US-0085714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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(HYSE-) HYSEQ INC.
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Ч
                                                                                                                                                                                                                                                                                                                                    11 AA;
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                                        ΦUH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200179449-A2.
                                      (LADD/) LADD A (WANG/) WANG C (ZAMB/) ZAMB T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
           27-APR-1993;
                    14-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-0CT-2001.
                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU30337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
AAU30337
   QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                           disease (GERD) that comprises administering to a patient an immunogenic composition which generates anti-gastrin antibodies, which bind to gastrin, in a patient; and administering histamine H_2 antagonist or a proton pump inhibitor. The method provides a more effective method for controlling acid output by the stromach. The therapy is less costly, High gastrin levels associated with standard therapies are neutralized and undesirable side effects are reduced. The method permits a reduced cosage of acid reducing agent both at the acid production of dosages is the acid production stimulating level (gastrin). Reduction of dosages is desirable for protonged treatment of GERD. In a combination therapy with H_2 agonists or proton pump inhibitors, anti-gastrin 17 antibody titers can be maintained by occasional boster shots while gastric acid the esophagitis to completely heal and no surgery is required. The present sequence represents a human tetratriacontagastrin (G34) immunogenic contagastrin (G34) immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helper T cell epitope; universal immune stimulator; invasin; hapten; gastrin; peptic ulcers; gastrin-stimulated tumours.
                                                                                                                                                                                                                    invention relates to the treatment of gastroesophageal reflux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                              Method for treatment of gastroesophageal reflux disease (GERD)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score.75; DB 21;
ilarity 100.0%; Pred. No. 0.00093;
Conservative 0; Mismatches 0;
                                                                                                                                        Michaeli D;
         /label= pGlu
/note= "pyroglutamate"
                                                                                                                                                                                                Example 4; Page 11; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR62738 standard; peptide; 11 AA.
                                                                                                                                        Karr S,
                                                                                                98US-0085610.
                                                                              99WO-US10734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94WO-US04832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                        Grimes S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ELGPOGRPPPPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ELGPQGRPPPPC 12
                                                                                                                    (APHT-) APHTON CORP.
                                                                                                                                                          WPI; 2000-062378/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gastrin hapten.
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-1995
                                                                                                15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-APR-1994;
                                                                             14-MAY-1999;
                                      WO9959612-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9425060-A
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                                                         25-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                      Gevas PC,
                                                                                                                                                                                                                                                                                                                                                                                                                           Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR62738;
                                                                                                                                                                                                                                                                                                                                                                                                       peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR62738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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synthetic immunogenic peptides are provided in which a universal immune stimulator is linked to a peptide or protein hapten containing B cell and/or cytotoxic T lymphocyte epitopes, giving a product which causes potent immune responses to the coupled peptide or protein. The stimulator consists of (A) a promiscuous helper T cell epitope (Th) which elicits an immune response to the coupled peptide in members of a heterogeneous population expressing diverse HLA phenotypes, and (B) an adjuvant peptide sequence from the invasin protein of Versinia. Spacer amino acid sequences (e.g. Gly-Gly) can be provided between the invasin and Th domains and between the immune stimulator and hapten components. When the hapten is LHRH, then optionally the invasin domain can be omitted from the immune stimulator component.

The present sequence is an example of a gastrin hapten which can be become the immune stimulator end hapten because the immune stimulator component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic luteinising hormone releasing hormone peptide(s) that suppress LHRH activity in males and females
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 56; DB 15; Length 11;
Pred. No. 0.29;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptic ulcer disease or gastrin-stimulated tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claims 27, 37; Page 96; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU30337 standard; Protein; 139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human secreted protein #828.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.7%;
81.8%;
93US-0057166.
94US-0229275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-2001; 2001WO-US08656
                                                                                                                                                                                                                                             Zamb T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 81.8'
                                                                                                                                                                                                                                                                                                                   WPI; 1994-357910/44.
                                                                                                                                                                                                                                                 Ladd AE, Wang CY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ELGPQGRPPPP 11
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1 QLGPQGPPPP 11
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AAO07572;
                                                                                                                                                                                                                                                                    Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAO07572
 δλ
                                                                                                                                                                                                                                                                                                                                                                                         qq
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                                                                                                                 polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration;
                             Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy \cdot
                                                                                                                                                                                                                                                                                                              bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias, AAU39510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel human secreted polypeptides. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                            invention relates to novel human secreted polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 279-280; 765pp; English.
                                                                            Claim 20; Page 279; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU30339 standard; Protein; 169 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human secreted protein #830.
                                                                                                                                                                                                                                                                                                                                                                                                                      73.38;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-APR-2001; 2001WO-US08656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-APR-2000; 2000US-0552929
26-JAN-2001; 2001US-0770160
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 72...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-611725/70.
WPI; 2001-611725/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ELGPQGRPPPP 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 QISPQGRPPPP 39
                                                                                                                                                                                                                                                                                                                                                                                         139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200179449-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                            Seguence
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polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopolesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAUS910-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the encoded proteins (AA000010-FAA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymetides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human polynucleotides (AAI79941-AAI93841) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. Leukaemia, inflammation and immune discreters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 21464; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 4.7; ; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA007572 standard; Protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polypeptide SEQ ID NO 21464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                73.3%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pang YT, Liu C, Drmanac RT;
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18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ELGPQGRPPPP 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       169 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAI87503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders
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S

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Gaps

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Indels

; 0 22;

Pred. No. 17; 2; Mismatches

Length 129;

DB

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66.7%; Score 50; 77.8%; Pred. No.
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (APHT-) APHTON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grimes S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1990-233029/31.
                                                      Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 AA;
                                                                                               3 GPQGRPPPP 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GPQGRPPPPC
                                                                                                               ||:|:||||
| GPKGKPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JAN-1989;
                                                                                                                                                                                                                                              07-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-APR-2000
                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990.
                                                                                                                                                                                                                                                                                                                                           EP380230-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gevas PC,
                                                                                                                                                                                                                     AAR06247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY51310;
                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                            AAR06247
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                                                                                                                       Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammatopoissis regulating activity, issue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytokine; cell proliferation; cell differentiation; gene therapy; vacchie; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID NO 14640; 1399pp + Sequence Listing; English.
                                                                                                                                                  Length 112;
                                                                                                                                                                           1; Indels
                                                                                                                                                  22;
                                                                                                                                            DB 7
                                                                                                                                                                            Mismatches
                                                                                                                                                Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                              AA000748 standard; Protein; 129 AA.
                                                                                                                                                                                                                                                                                                                                                                              Human polypeptide SEQ ID NO 14640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RT;
                                                                                                                                               66.78;
88.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                  06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT, Liu C, Drmanac
                                                                                                                                                                        8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-514838/56.
                                                                                                                                                            Best Local Similarity
                                                                                                                    112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                            57
                                                                                                                                                                                                    3 GPQGRPPPP 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAI80679
                                                                                                                                                                                                                              49 GPQGGPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-2001.
                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                         AAO00748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders
                                                                                                                                                Query Match
                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                    RESULT 9
AAO00748
                                                                                                                                                                                                                                                                                                            888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogens against gastrin peptide(s) - used to induce antibodies that specifically neutralise single form of gastrin, G17 or G34 \,
                                                                                                                                                                                                                             Gastrin; tumours; peptic ulcers; diptheria toxoid; tetanus toxin;
                                                                                                                                                   Antigenic peptide fragment selected from the 12 N-terminal AAs heptadecagastrin (G17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigenic fragments may be attached to an immunogenic carrier and used to raise Abs to a specific single form of Gastrin ie. G17 or G34. Peptide fragments capable of binding to these Abs are useful in neutralising anti-gastrin Abs in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.3%; Score 49; DB 11; Length 11; 80.0%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Littenberg RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gastrin G17 derived immunogen hG17(5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
AAR06247 standard; protein; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY51310 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page 19; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Karr SL,
                                                                                                                                                                                                                                                                                                                                                                                  90EP-0300456
                                                                                                                                                                                                                                                                                                                                                                                                                                  89US-0351193
                                                                                                                                                                                                                                                                                                                                                                                                                                                          89US-0301353
                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY51310
ID AAX5
XX
XX
DT 14-A
XX
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 Hume
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KW Immu
KW Perr
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us-09-700-329-2.rag

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3 GPQGRPPPPC 12
                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                             11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAI80461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-SEP-2001
                          Gevas PC,
                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                AAO00530;
                                                                                                                                                                                                                                            peptides
                                                                                                                                                                                                                                                                                                                                                             RESULT 13
ÖΣ
                                                                                                                                                                                                                                                                                                                               Db
                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                             This invention describes a novel method for the treatment or preventing hypergastrinemia by administering to a patient a gastrin G17 and/or G34 peptide fragment linked by an amino acid spacer to an immunogenic carrier. The methods are used to treat hypergastrinemic patients, particularly those with pernicious anemia, those receiving treatment with anti-ulcer agents such as proton pump inhibitors (particularly omeprazole or lansoprazole) or H_2 receptor blocking agents or antagonists, or those having colorectal disorders or diseases. This sequence represents a human gastrin G17 derived immunogen which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gastroesophageal reflux disease; GERD; gastrin; anti-gastrin antibody; histamine H_2; proton pump inhibitor; acid output; stomach; therapy; esophagitis; immunogen; human; heptadecagastrin; G17.
                                                                                                                                                    Treating or preventing hypergastrinemia comprising administration of, e.g. antl-gastrin antibodies
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                 65.3%; Score 49; DB 21; Length 11; 80.0%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                  ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human heptadecagastrin (G17) immunogenic peptide 2.
                                                                                                                  Watson
                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                  Michaeli D,
                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _label= pGlu
/note= "pyroglutamate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  AAY49304 standard; peptide; 11 AA.
                                                                                                                                                                             Example 3; Page 18; 44pp; English.
                                                                                                                  Karr S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US10734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0085610
                                                            99WO-US10751
                                                                              98US-0085714
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                  Grimes S,
                                                                                                (APHT-) APHTON CORP.
                                                                                                                                  WPI; 2000-116301/10
                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                     3 GPQGRPPPPC 12
                                                                                                                                                                                                                                                                                                                                                                     2 GPWLRPPPPC 11
                                                                                                                                                                                                                                                                                               11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
         Homo sapiens
                          W09959631-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09959612-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAY-1999;
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                                                            14-MAY-1999;
                                                                              15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAR-2000
                                            25-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-NOV-1999
                                                                                                                  Gevas PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY49304;
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        AAY49304
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The invention relates to the treatment of gastroesophageal reflux disease (GERD) that comprises administering to a patient an immunogenic composition which generates anti-gastrin antibodies, which bind too gastrin, in a patient; and administering histamine H.Z antagonist or a proton pump inhibitor. The method provides a more effective method for controlling acid output by the stomach. The therapy is less costly. High gastrin levels associated with standard therapies are neutralized and undesirable side effects are reduced. The method permits a reduced dosage of acid reducing agent both at the acid producing level as well as the acid production stimulating level (gastrin). Reduction of dosages is desirable for prolonged treatment of GERD. In a combination therapy with H.Z agonists or proton pump inhibitors, anti-gastrin 17 antibody titers can be maintained by occasional booster shots while gastric acid inhibitor dosing is reduced. Immunization allows a sufficient time for the esophagitis to completely heal and no surgery is required. Sequences AAV43303-306 represent human heptadecagastrin (G17) immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                 Method for treatment of gastroesophageal reflux disease (GERD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB 21; Length 11; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                    Michaeli D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAO00530 standard; Protein; 146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polypeptide SEQ ID NO 14422.
                                                                                                                                                                                                                                                                                              Example 4; Page 11; 24pp; English
                                                                    Karr S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.3%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 80..
89.
                                                                    Grimes S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-514838/56.
(APHT-) APHTON CORP.
                                                                                                                                         WPI; 2000-062378/05
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Wed Feb

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The invention relates to human polynuclectides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynuclectides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecules encoding 62 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; nootropic; antibacterial; virucide; fungicide; opthalmalogical; human; vulnerary; gene therapy; infection; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fragment of human secreted protein encoded by gene 19 clone HTADW91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birse CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shi Y;
Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g., leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAB38321-B38396 represent the amino acid sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                 Claim 20; SEQ ID NO 14422; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soppet DR,
Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA, Sa
Florence KA,
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                Score 49;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB38442 standard; peptide; 383 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 55; 716pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Komatsoulis GA,
n HS, Ebner R,
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
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Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-647418/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 LGPPGAPPPP 124
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LGPQGRPPPP 11
                                                                                                                                                                                                                                                                                                                                               146 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lafleur DW,
                                                                                                                                                                                                                                                                                                                                              Sequence
                                   disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
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62

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W Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
W antibiflammacrory; antirheumatic; antiarthritic; immunosuppressive;
W antibacterial; endocrine; cardiant; central nervous system; virucide;
W antibacterial; endocrine; cardiant; cantianeemic; anaemia;
W antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
W antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; czeema;
W dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
N neuroprotective; antidepressant; nootropic; antidabetic; cytostatic;
N immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
W antianaphylactic; rheumatolid arthritis; septic shock; pancreatitis;
W antianaphylactic; neuropathology; cardiac anaphylaxis; autoimmunity;
W hombocytopaenia; osteoporosis; severe combined immunodeficiency;
W hirombocytopaenia; osteoporosis; severe combined immunodeficiency;
W hirombocytopaenia; osteoporosis; severe combined immunodeficiency;
W hirombocytopaenia; parkinson's disease; neurodegenerative disorder;
human secreted proteins encoded by the genes AAC69512-C69587. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) autoinmune diseases e.g. rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms of the breast or liver; (c) cardiovascular disorders e.g. cardiac arrest; (d) cerebrovascular disorders e.g. cerebmia; (e) anglogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g) incertons caused by bacteria, viruses and fungi; and (h) ocular
                                                                                                                                                                                                                            disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in
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Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein sequence SEQ ID NO:1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM25613 standard; Protein; 383 AA.
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80.0%;
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2000US-0488725.
2000US-0553317.
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N-PSDB; AAH99554.
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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5 LGPPGSPPPP 14
                                                                                                                                                                                                                                                                                                                                                       383 AA;
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21-JAN-2000;
25-APR-2000;
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                                                                                                                                                                                                                                                                                                                chemotaxis
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reatment and diagnosis of e.g. cancer, ulcers and HIV infection - XX

Claim 20; Page 234; 1217pp; English.

XX

Claim 20; Page 234; 1217pp; English.

CC AAM25963. The proteins can have activities based on the tissues and cclaim they are expressed in, such as: antinfinamatory; antirhematic; cardiant; cardiant; cardiant; cardiant; antianeamic; antinfinamatory; antirhematic; cardiant; cardiant; antianeamic; antiallergic; antimutagen; cardiant; cardiant; antianeamic; antiallergic; antimutagen; cardiantic; cardiant; dermatological; antiallergic; antimutagen; cardiantic; cardianeamic; antiallergic; antiallergic; unterary; antidiabettc; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetti; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetti; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetti; cytostatic; neuroprotective; antidepressant; nootropic; cantidiabetti; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetti; cytostatic; neuroprotective; antidepressant; nootropic; cantidation; The proteins and polynucleotides are useful for screening for production, The proteins and polynucleotides are useful for screening for disorders associated with the activity of a protein e.g. inflammation, creamatol arthritis, septic shock, pancreatitis, cardiac dysfunction, infections, autoimmunity, genetic diseases, heamatopoietic disorders, cancer, multiple solerosis, depression, consemporosis, severe combined immunodeficiency, eczema, allergic continuitis, asthma, diabetes, cancer, multiple solerosis, depression, continuitis, asthma, diabetes, cancer, multiple solerosis, depression, continuity, and disorders, multiple solerosis, depression, continuities, asthma, diabetes, mandamic, mercodegenerative and continuity and
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Search completed: February 5, 2003, 09:47:57 Job time : 36.4286 secs

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Gaps

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65.3%; Score 49; DB 22; Length 383; 80.0%; Pred. No. 62; 2; Indels Live 0; Mismatches 2; Indels

Query Match
Best Local Similarity 80.03
Matches 8; Conservative

2 LGPQGRPPPP 11 ||| | |||| 5 LGPPGSPPPP 14

9 9

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February 5, 2003, 09:46:31; Search time 15.4286 Seconds (without alignments) 74.771 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                    283224 seqs, 96134422 residues
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1 ELGPQGRPPPPC 12
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	pt	collagen alpha 1/x		conserved hypothet	hypothetical prote	_	-+-	requiatory protein	capsid protein - h	collagen alpha 2(X	HD protein - mouse	al		hypothetical profe	Q.	transcription fact	homeotic protein H	hypothetical prote	collagen alpha 27V	hypothetical profe	collagen alpha 2/V	exopolysaccharide	alpha	collagen alpha 1(X	collagen alpha 1(x	basic proline-rich	proline-rich prote	proline	hypothetical prote		
SUMMARIES	ID	00	В	T02857	9	0	23	T13425	WMBEW6	CGHU2E	149729	D72654	A33509	T47181	B84565	150589	S35941	T23561	A24450	T10216	A57131	S74742	A32856	S18251	\pm	C38355	D40750	D38355	A86441	3629	
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ф	Query	66.7	65,3	65.3	64.0	64.0	64.0	62.7	62.7	62.7	62.7	61.3	61.3	0.09	0.09	0.09	0.09	0.09	0.09	0.09	60.09	0.09	0.09	0.09	0.09	58.7	58.7	58.7	58.7	58.7	
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E4 protein - human salivary proline-r	salivary proline-r salivary proline-r rhodosin - Allote	rhodopsin (similar rhodopsin - northe	transcription fact still frameshift 3 hypothetical prote	hypothetical prote hypothetical prote	inforcing proce transcription acti collagen alpha 1(V
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ALIGNMENTS

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Total number of hits satisfying chosen parameters:

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C;Accession: T32976
R;Bentley, D.; Le, T.T.
Submitted to the EMBL Data Library, February 1998
A;Description: The sequence of C. elegans cosmid F57H12.
A;Reference number: Z1258
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A;Cross-references: EMBL:AF003139; PIDN:AAB54156.1; GSPDB:GN00019; CESP:F53G12.7
A;Experimental source: strain Bristol N2; clone F53G12
C;Genetics:
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T29031
R;Wu, X.; Graves, T.

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C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 17-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F57H12.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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15;
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     Mismatches
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A;Introns: 59/3; 138/1; 223/2
C;Superfamily: unassigned collagens
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Best Local Similarity 72.7.
Loc 8; Conservative
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Matches 7; Conservative
          Conservative
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260 EMGPQGPPGPP 270
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1855 PRGCPPPPC 1863
                                                                                                             4 PQGRPPPPC 12
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A; Introns: 30/3; 159/3
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NiAlternate names: 1.7 S seed storage protein
C;Species: Brassica napus (rape)
C;Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 16-Jul-1999
C;Accession: A29802
C;Accession: A29802
E;Scofield, S.R.; Crouch, M.L.
J. Biol. Chem. 262, 12202-12208, 1987
A;Title: Nucleotide sequence of a member of the napin storage protein family from Brassi A;Reference number: A29802; MUID:87308225; PMID:3040733
A;Accession: A29802
A;Access
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-2241 <PYL>
A;Residues: 1-2241 <PYL>
A;Cross-references: GB:AE001274; NID:93264850; PIDN:AAC24680.1; PID:93002479; GSPDB:GNOG
A;Experimental source: strain MHOM/IL/81/Friedlin
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C;Species: Leishmania major
C;Species: Leishmania major
C;Species: Leishmania major
C;Accession: E81463; T02857
R;Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.; Froc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome l has an unusual distribution of protein-c A;Reference number: A81455; MuID:99178987; PMID:10077609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein L3162.1 [imported] - Leishmania major (strain Friedlin)
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F;539-541/Region: cell attachment (R-G-D) motif
F;572-630/Domain: collagenous COL7 #status predicted <COL7>
F;652-722/Domain: collagenous COL6 #status predicted <COL6>
F;652-722/Domain: collagenous COL6 #status predicted <COL6>
F;738-875/Domain: collagenous COL3 #status predicted <COL5>
F;887-938/Domain: collagenous COL3 #status predicted <COL4>
F;887-938/Domain: collagenous COL3 #status predicted <COL4>
F;1005-1007/Region: cell attachment (R-G-D) motif
F;1011-1432/Domain: collagenous COL2 #status predicted <COL2>
F;1226-1228/Region: cell attachment (R-G-D) motif
F;1472-1577/Domain: collagenous COL1 #status predicted <COL1>
F;1578-1603/Domain: carboxyl-terminal nonhelical #status predicted
F;1578-1603/Domain: carboxyl-terminal (Covalent) #status predicted
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C;Superfamily: Leishmania major probable membrane protein L3162.1
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Pred. No. 96;
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Pred. No. 52;
1; Mismatches 1; Indels
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Pred. No. 9.6;
0; Mismatches 1; Indels
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Best Local Similarity 88.9%;
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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1280 MGPQGRPGPP 1289
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Best Local Similarity
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A; Reference number: A30083; MUID:88274327; PMID:2839594
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77.8%;
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A; Residues: 586-1546 <KIM>
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Best Local Similarity
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A; Molecule type: mRNA
A; Residues: 1-663 <ZHI>
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                              A; Accession: H30084
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R;McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; Perr J. Gen. Virol. 69, 1531-1574, 1988
A;Title: The complete DNA sequence of the long unique region in the genome of herpes sim
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                     R;Stadler, H.S.; Padanilam, B.J.; Buetow, K.; Murray, J.C.; Solursh, M. Proc. Natl. Acad. Sci. U.S.A. 89, 11579-11583, 1992
A;Title: Identification and genetic mapping of a homeobox gene to the 4p16.1 region of A;Reference number: A47234, MUID:93087572, PMID:1360670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribrost, E.; Deryckere, F.; Roos, C.; Haenlin, M.; Pantesco, V.; Mohier, E. Genes Dev. 2, 891-900, 1988
A:Title: Role of the occyte nucleus in determination of the dorsoventral polarity of A; Reference number: A28826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulatory protein K10, oocyte-specific - fruit fly (Drosophila melanogaster) NAtternate names: protein E6:3088.5 C;Species: Drosophila melanogaster C;Becies: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999 C;Accession: T13425; A28826 K;Murphy, L.; Harris, D.; Barrell, B. submitted to the EMBL Data Library, April 1999 A;Becription: Sequencing the distal X chromosome of Drosophila melanogaster. A;Reference number: 217668
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C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000
                                                                                                                                                                                                       A; Residues: 1-373 <STA>
A; Experimental source: embryo craniofacial region
A; Mote: sequence extracted from NCBI backbone (NCBIN:119953, NCBIP:119955)
C; Superfamily: unassigned homeobox proteins; homeobox homology
C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
F; 201-257/Domain: homeobox homology <HOX>
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A; Residues: 1-276, 'HH', 279-281, 'VDHHR', 287-463 <PRO>
A; Cross-references: GB:X12836; NID:98148; PID:9295771
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25;
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Pred. No. 41;
1; Mismatches
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Pred. No. 2
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A;Molecule type: DNA
A;Residues: 1-463 <MUR>
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77.8%;
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70.0%;
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A; Residues: 1-373 <STA>
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278 MGPMGGPPPP 287
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Best Local Similarity
Matches 7; Conser
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Best Local Similarity
Matches 7; Conserv
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  C; Accession: A47234
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                                                                                                                                A; Accession: A47234
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A; Introns: 432/3
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A'Poscription: structural component of extracellular fibrous polymer associated with A'Note: may play a role in controlling the lateral growth of collagen II fibrils C'Superfamily: collagen alpha I(V) fondin; fibrillar collagen alpha I(V) fondin; fibrillar collagen alpha I(V) fondin; fibrillar collagen alpha I(V) fondin; glycoprotein; hydroxylysine; hydroxypr F;1-254/Domain: non-collagenous (fragment) #status predicted <NC3>
F;1-254/Domain: non-collagenous (fragment) #status predicted <NC3>
F;1-355-305/Domain: collagenous #status predicted <NC2>
F;345/Domain: collagenous #status predicted <NC2>
F;345/Aggion: cell attachment (R-G-D) motif F;447-449/Region: cell attachment (R-G-D) motif F;1357-1159/Region: cell attachment (R-G-D) motif F;1357-1159/Region: cell attachment (R-G-D) motif F;1357-1159/Region: carboxyl-terminal nonhelical telopeptide F;1381-1546/Domain: carboxyl-terminal propeptide (fragment) #status predicted <CTP>
F;1381-1546/Domain: carboxyl-terminal propeptide (fragment) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N'Alternate names: procollagran alpha 2(XI) chain N'Contains: procollagran alpha 2(XI) chain N'Contains: proline/arginine-rich protein (PARP) (Species: Homo sapiens (man) C. Date: 07-Jun-1990 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999 (SACCESSION: S34790; A32645 FRES Lett. 326, 25-28, 1993 *A31645 FRES Lett. 326, 25-28, 1993 *A31tle: Molecular cloning of PARP (proline/arginine-rich protein) from human cartila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Cross-references: GDB:119788; OMIM:120290
A.Map position: 6p21.3-6p21.3
A.Introns: 1302/3: 1332/3: 1332/3: 1440/1: 1477/3
A.Note: the list of introns is incomplete
C.Complex: type XI collagen may be a heterotrimer of two alpha 1(XI) chains (see PIR: 3(XI) chain (see PIR: GGHGC), initially linked by disulfide bonds among their carbox raned with desmosine cross-links made from lysine and allysine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Note: parts of this sequence were determined by protein sequencing C;Comment: Prolines and lysines at the third position of the tripeptide repeating unied and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecular cloning of cDNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: EMBL:L18987; NID:g306439; PIDN:AAA35498.1; PID:g306440
R;Kimura, T.; Cheah, K.S.E.; Chan, S.D.H.; Lui, V.C.H.; Mattei, M.G.; van der Rest, J. Biol. Chem. 264, 13910-13916, 1989
A;Title: The human alpha2(XI) collagen (COLIAA2) chain. Molecular cloning of CDNA an A;Reference number: A32645; MUID:89340485; PMID:2760050
                                                                                                                                                     A; Cross-references: GB:X14112; NID:91944536; PIDN:CAA32318.1; PID:959526; GB:D00317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-635 <MCG>
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             collagen alpha 2(XI) chain precursor - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: S34790; MUID: 93314796; PMID: 8325374
                                                                                                                                                                                            C'Genetics:
A;Gene: UL26
C;Superfamily: varicella-zoster virus gene 33 protein
C;Keywords: capsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47;
Pred. No.
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Σ

Gaps

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A)Cross-references: GB:J04804
C;Superfamily: meta-vinculin; vinculin amino-terminal homology; vinculin carboxyl-ter
C;Keywords: actin binding; cytoskeleton
F;4-257/Domain: vinculin amino-terminal homology <VINN>
F;477-1007/Domain: vinculin carboxyl-terminal homology <VINC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable spliceosome associated protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
C;Accession: B84565
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein DKFZp434F0616.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 08-Dec-2000
C;Accession: T47181
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, March 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 01-Mar-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: A33509
R;Barstead, R.J.; Waterston, R.H.
J. Biol. Chem. 264, 10177-10185, 1989
A;Title: The basal component of the nematode dense-body is vinculin. A;Reference number: A33509; MUID:89255506; PMID:2498337
A;Accession: A33509
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                      Indels
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                  .;
5
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                  Mismatches
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Pred. No.
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C; Superfamily: POZ domain homology
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A Accession: T47181
A Status: preliminary
A Molecule type: mRNA
A Residues: 1-315 <AAA>
A Cross-references: EMBL:AL162003
                                                                                                                                                                                                                                                                                                                                                                                                        vinculin - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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72.7%;
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Best Local Similarity 72.7
Matches 8; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1010 <BAR>
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                                                                                                       4 PQGRPPPPC 12
                                                                                                                                                                                         71 POSRPPSPC 79
                  7;
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B84565
                  Matches
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D72654
hypotherical protein APE0664 - Aeropyrum pernix (strain KI)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: D72654
R:Kawarabayasi, Y: Hino, Y: Horikawa, H:; Yamazaki, S.; Haikawa, Y:; Jin-no, K.; Takah awa, H:; Takamiya, M:; Masuda, S:; #unahashi, T:; Tanaka, T:; Kudoh, Y:; Jin-no, K.; Takah awa, H:; Takamiya, M:; Bonome sequence of an aerobic hyper-thermophilic Crenarchaeon, A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A:Reference number: A72450; MUID:99310339; PMID:10382966
A; Accession: D72654
A; Molecule type: DNA
A; Residues: 1-112 < KAM>A; Residues: 1-112 < KAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H9 protein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 149729; 149720
C;Accession: 149729; 149730
R;Lin, B.; Nasir, J.; MacDonald, H.; Hutchinson, G.; Graham, R.; Rommens, J.M.; Hayden, Hum. Mol. Genet. 3, 85-92, 1994
A;Tille: Sequence of the murine huntington disease gene: evidence for conservation and a A;Reference number: 149729; MUID:94214482; PMID:8162057
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 149730
A;Access
F;109-163,1511-1545/Disulfide bonds: #status predicted
F;319/Modified site: allysine (Lys) #status predicted
F;326/Modified site: Approxylysine (Lys) #status predicted
F;426,1266/Modified site: Carbohydrate (Lys) (covalent) #status predicted
F;927,933,1008,1017,1035,1038,1290,1296,1305,1317,1320/Modified site: 4-hydroxyproline (Fys) #status atypical
F;929/Modified site: A-hydroxyproline (Fro) #status atypical
F;942,1023,1299/Modified site: carbohydrate (Lys) (covalent) #status experimental
F;1427,1433,1450,1459/Disulfide bonds: interchain #status predicted
F;1460/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.7%; Score 47; DB 1; Length 1546; 80.0%; Pred. No. 1.3e+02; 1ve 0; Mismatches 2; Indels
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Pred. No. 15;
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87.5%; Pred. No. 2.4e+02;
iive 1; Mismatches 0
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77.8%;
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Best Local Similarity 80.0
Matches 8; Conservative
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nes 7; Conserv
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45 PQGQPPPP 52
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Matches
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Nature 402, 761-768, 1999

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transcription factor - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: 13-599-1996 #sequence_revision 13-Sep-1996 #text_change 19-Jul-2002
C;Accession: 150589
R;Prince, V.; Lumsden, A.
Development 120, 911-923, 1994
A;Title: hoxa-2 expression in normal and transposed rhombomeres: independent regulation
A;Reference number: 150589; MUID:95324377; PMID:7600967
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary;
A;Rossidues: 1.375 cPRID
A;Cross-references: EMBL:X74323; NID:9415799; PIDN:CAA52370.1; PID:9415800
C;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: homeotic protein Hox B2; homeobox homology
C;Keywords: DNA binding; homeobox, nucleus; transcription regulation
F;141-197/Domain: homeobox homology <a href="https://www.nucleus">homeobox homology 
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUD:20083487; PMID:10617197
A:Reference number: A84420; MUD:20083487; PMID:10617197
A:Reference number: B4565
A:Residues: preliminary
A:Residues: 1-363 <STO>
A:Rolecule type: DNA
A:Residues: 1-363 <STO>
A:Cross-references: GB:AE002093; NID:94218014; PIDN:AAD12222.1; GSPDB:GN00139
C:Genetics: A:Gene: At2918510
A:Map position: 2
C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotei
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 GenCore version
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Length 351;

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Score 51;

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Query Match

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MEDLINE-96025976; Pubmed-7565748;
Anderson K. P., Kern C.B., Crable S.C., Lingrel J.B.;
Anderson K. P., Mern C.B., Crable S.C., Lingrel J.B.;
Anderson K. P. Mern C.B., Crable S.C., Lingrel J.B.;
homologous to erythroid Kruppel-like factor: identification of a new multigene family.
i-1.5957-5965(1995).
i-1.FUNCTION: BINDS TO THE CACC BOX IN THE BETA-GLOBIN GENE PROMOTER
AND ACTIVATES TRANSCRIPTION.
i-2 SUBCELLULAR LOCATION: Nuclear (By similarity).
i-1.SSUE SPECIFICITY: PREDOMINANT EXPRESSION IN THE LUNGS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC; T01677; ...
MGD; MGI:1342772; K1f2.
MGD; MGI:1342772; K1f2.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; Z1-C2H2; 3.
PRINTS; PR000048; Z1NCFINGER.
ProDom; PD000003; Znf_C2H2; 2.
SMART; SM00365; ZnF_C2H2; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Transcription regulation; Activator; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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Pred. No. 5.9;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C4A99D018AC5BAF7 CRC64;
                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Kruppel-like factor 2 (Lung kruppel-like factor).
                                                                                                                                                                                                           354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-ALA.
ZINC FINGERS.
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POLY - PRO.
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                                                                                                                                                                                                           PRT;
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353
295 C2
325 C2
353 C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U25096; AAA86728.1; -.
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88.9%;
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                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-binding; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FINGER PROTEINS.
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                                    || ||||||
160 GPAGRPPPP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
3 GPQGRPPPP 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                       KLFZ OR LKLF.
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                                                                                                                                                                                                        KLF2_MOUSE
Q60843;
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ZN_FING
ZN_FING
SEQUENCE
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Best Local (
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                                                                                                                                                                               KLF2_MOUSE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kisselev L.L.;
"Structure of the human CpG-island-containing lung Kruppel-like factor (LKLF) gene and its location in chromosome 19p13.11-13 locus.";
FBBS Lett. 448:149-152(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Lee H.J., Kim M.K., Kim Y.H., Seo J.M., Lee H.M., Chung H.J.,
Sohn M.Y., Hwang S.Y., Im S.U., Jung E.J., Kim J.C.;
Sohn M.Y., Hwang S.Y., In the human dermal papilla cells as identified
by expressed sequence tags.";
Submitted (Nov-1999) to the EMBL/GenBank/DBBJ databases.

-i- FUNCTION: BINDS TO THE CACCC BOX IN THE BETA-GLOBIN GENE PROMOTER
AND ACTIVATES TRANSRIPTION (BY SHILLARLY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wani M.A., Conkright M.D., Jeffries S., Hughes M.J., Lingrel J.B.; "CDNA isolation, genomic structure, regulation, and chromosomal localization of human lung kruppel-like factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
FINGER PROTEINS.
                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pfam; PF00096; Zf_C2H2; 3.
Probom; PR000003; Znf_C2H2; 3.
SMART; SM00355; ZnF_C2H2; 3.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Transcription regulation; Activator; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99231781; PubMed=10217429;
Kozyrev S.V., Hansen L.L., Poltaraus A.B., Domninsky D.A.,
                            Q9Y5W3: Q9UKR6; Q9UJS5;
30-MAY-2000 (Rel. 39, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Kruppel-like factor 2 (Lung kruppel-like factor).
KLF2 OR LKLF.
355 AA
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POLY-GLY.
POLY-PRO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99389728; PubMed=10458913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AF123344; AAD25076.1; -. EMBL, AF134053; AAD55891.1; -. EMBL, AF205849; AAF13295.1; -. HSSP; P08047; 1SP2. TRANSFAC; T04958; -.
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics 60:78-86(1999).
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MIM; 602016; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RX TESUS=Placenta;

RX MEDLIN=9303161; PubMed=1284248;

RA MEDLIN=93203161; PubMed=1284248;

RA Ranamori T., Yammakoshi H., Nagai Y.;

RA Ranamori T., Yammakoshi H., Nagai Y.;

RA Ranamori T., Yammakoshi H., Nagai Y.;

RT "Molecular cloning and partial characterization of a novel collagen

RT "Molecular cloning and partial characterization of a novel collagen

RT chain, alpha 1(XVI), consisting of repetitive collagenous domains and

RT Chain, alpha 1(XVI), consisting of repetitive collagenous domains and

RT Chain, alpha 1(XVI), consisting of repetitive collagenous domains and

RT This Molecular cloning non-collagenous segments.";

CC -: FUNCTION: THE NUMBROUS INTERRUPTIONS IN THE TRIPLE HELIX MAY MAKE

CC -: FUNCTION: THE NUMBROUS INTERRUPTION IN THE PLACENTA, WHERE IT IS FOUND IN THE AMMION, A MEMBRANOUS TISSUE LINING THE AMMION A REBREATH THIS DENSE LAYER. EXISTS IN TISSUES IN ASSOCIATION

CC -: DEVELOPMENTAL STARES: TRANSIENTLY ELEVATED EXPRESSION DURING

GESTATION, AND DECREASE AT TERM.

CC -: DOWAIN: THIS SEQUENCE DEFINES EIGHTEEN DOMAINS, NINE

CC -: TRIPLE HELICAL DOMAINS (COL9 TO COL1) AND TEN NONTRIPLE-HELICAL
                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-he European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAINS (NCIO TO NCI).

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH, INTERRUPTED HELICES (FACIT) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92335339; PubMed-1631157; Martel M.-G., Timpl R., Chu M.-L.; Lang R.Z., Mattel M.-G., Timpl R., Chu M.-L.; Cloning and chromosomal location of human alpha 1(XVI) collagen."; Proc. Natl. Acad. Sci. U.S.A. 89:6565-6569(1992).
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                     ;
0
                                                                                                                                          Score 50; DB 1; Length 355;
Pred. No. 7.9;
Mismatches 1; Indels
          ZINC FINGERS.

C2H2-TYPE.

C2H2-TYPE.

C2H2-TYPE.

S - N (IN REF. | 2).

L - P (IN REF. 2).

L - M (IN REF. 2).

L - M (IN REF. 2).

L - M (IN REF. 2).

M; D5849C83ID676AEI CRC64;
                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Collagen alpha 1(XVI) chain precursor.
                                                                                                                                                                                                                                                                                    PRT; 1603 AA
                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 418-1603 FROM N.A. TISSUE=Placenta;
                                                                                                                  37419 MW;
                                                                                                                                          66.7%;
88.9%;
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                   STANDARD;
 3354
354
354
354
104
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
225
272
272
332
43
104
175
184
                                                                                                                                          Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                         162 GPGGRPPPP 170
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SEQUENCE FROM N.A.
                                                                                                                                                                                            3 GPQGRPPPP 11
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Q07092;
                                                 ZN_FING
CONFLICT
CONFLICT
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ZN_FING
 DOMAIN
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Prassica napus (Rape).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                         Pfam; PF01391; Collagen; 18.
Pfam; PF02210; TSPN; 1.
SMART; SM00210; TSPN; 1.
Extracellular matrix; Connective tissue; Collagen; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Napin embryo specific precursor (1.7S seed storage protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRIPLE-HELICAL REGION 3 (COL3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRIPLE-HELICAL REGION 2 (NC2),
WITH 2 IMPERECTIONS.
                                                                                                                                                                                                                                                                                                                                                                        NONHELICAL REGION 7 (NC7).
TRIPLE-HELICAL REGION 6 (COL6)
WITH 1 IMPERFECTION.
NONHELICAL REGION 6 (NC6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NONHELICAL REGION 5 (NC5).
TRIPLE-HELICAL REGION 4 (COL4)
                                                                                                                                                                                                             COLLAGEN ALPHA 1(XVI) CHAIN.
NONHELICAL REGION 10 (NC10).
TRIPLE-HELICAL REGION 9 (COL9)
                                                                                                                                                                                                                                                                                                                          NONHELICAL REGION 8 (NC8).
TRIPLE-HELICAL REGION 7 (COL7)
                                                                                                                                                                                                                                                                                                                                                                                                                                          TRIPLE-HELICAL REGION 5 (COL5) WITH 3 IMPERFECTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NONHELICAL REGION 3 (NC3).
TRIPLE-HELICAL REGION 2 (COL2)
                                                                                                                                                                                                                                                                                           TRIPLE-HELICAL REGION 8 (COL8) WITH 1 IMPERFECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1603;
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R -> P (IN REF. 2).

T -> P (IN REF. 2).

T -> P (IN REF. 2).

T -> P (IN REF. 2).

S -> P (IN REF. 2).

MW; E27D9AID4E598A37 CRC64;
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RDA -> GGR (IN REF. 2).
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                                                                                                                                                                                                                                                                              (NC9)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50;
Pred. No.
                                                                            InterPro; IPR000087; Collagen.
InterPro; IPR003129; TSPN.
EMBL; M92642; AAA58427.1; -. EMBL; S57132; AAB25797.1; -.
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                           PIR; $23810; $23810.
Genew; HGNC:2193; COL16A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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418
537
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22
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                                                           MIM; 120326; -
                                                                                                                                                                             Repeat; Signal
SIGNAL
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CONFLICT
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SEQUENCE
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CONFLICT
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or send an email to license@isb-sib.ch).
                                                                                                J. Biol. Chem. 262:12202-12208(1987).

- PUNCTION: THE SMALL, BASIC, WATER-SOLUBLE NAPINS ARE ONE OF THE TWO MAJOR KINDS OF STORAGE PROTEINS SYNTHESIZED IN THE SEED DURING ITS MATURATION.
                                                                                                                                                                                        -i- SUBUNIT: THE MATURE PROTEIN CONSISTS OF A SMALL AND A LARGE CHAIN LINKED BY DISULFIDE BONDS.
-i- TISSUE SPECIFICITY: COTYLEDONS AND THE AXIS.
-i- DEVELOPMENTAL STAGE: EMBRYO.
-i- SIMILARITY: BELONGS TO THE 2S SEED STORAGE ALBUMINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                        Scoffeld S.R., Crouch M.L.; "Nucleotide sequence of a member of the napin storage protein family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Role of the oocyte nucleus in determination of the dorsoventral polarity of Drosophila as revealed by molecular analysis of the K10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.3%; Score 49; DB 1; Length 186; 88.9%; Pred. No. 5.9; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prost E., Deryckere F., Roos C., Haenlin M., Pantesco V.,
Mohier V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LARGE CHAIN.
9CAE63D84B160AB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K10_DROME STANDARD; PRT; 463 AA. P13_468; 046075; 09M505; 01-JAN-1990 (Rel. 13, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 16-JUL-1998 (Rel. 36, Last sequence update) 16-JUL-1999 (Rel. 40, Last annotation update) PNA-binding protein K10 (Female sterile protein K10). FS(1)K10 OR EG:30B8.5 OR CG3218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR0013612; AAI.
InterPro; IPR0010617; Napin.
InterPro; IPR001068; Try/amyl_mhbtr.
Prem; PR00134; try/amyl_mhbtr.
PRINTS; PR00496; NAPIN.
ProDom; PD002498; Napin; 1.
SmART; SM00499; AAI; 1.
SmART; Sprotein; Signal; Multigene family.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMALL CHAIN.
                 MEDLINE-87308225; PubMed-3040733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21013 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J02782; AAA33007.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 65.3
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A29802; A29802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
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  SOUR DEPT TO THE PET T
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RAY MEDILINE-2016/011, PubMed-10/31137;
Renots Paralle 16. Ferra C. Vuldal S., Brun C.; Demailles J., Godden E.,
Ray Marrell 18. G., Ferra C. Vuldal S., Brun C.; Demailles J., Godden E.,
Ray Marrell 18. G., Ferra C. Vuldal S., Brun C.; Demailles J., Godden E.,
Ray Medical Marrell 18. G., Ferra C., Vuldal S., Brun C.; Demailles J., Godden E.,
Ray Medical Marrell 18. G., Ferra C., Vuldal S., Brun C.; Demailles J., Godden E.,
Ray Medical Marrell 18. G., Ferra C., Vuldal S., Brun C., Demailles J., Godden E.,
Ray Medical Marrell 18. G., Ferra C., Schert C., Brun C., Demaille S., Godden E.,
Ray Medical Marrell 18. G., Ferra C., Schert C., Brun C., Brunders R.D.C.,
Glover D.M., Campbell L.A., Delamitsou A., Henderson N.S.,
Ray Medical Marrell 18. G., Ferra C., Schert E., Marrell 18. G., Schert S., E., ILP 78. Holt R.A., Walent I.P., Saunders R.D.C.,
Ray Marrell 18. G., Schert S.E., ILP 78. Hoskits R.A., Galle R.F.,
Ray Medical Marrell 18. G., Schert S.E., ILP 78. Hoskits R.A., Galle R.F.,
Ray Medical Marrell 18. G., Schert S.E., ILP 78. Hoskits R.A., Galle R.F.,
Ray Marrell 19. G., Schert S.E., ILP 78. Hoskits R.A., Galle R.F.,
Ray Marrell 19. G., Schert S.E., ILP 78. Hoskits R.A., Galle R.F.,
Ray Marrell 28. G., Schert S.E., ILP 78. Hoskits R.A., Galle R.F.,
Ray Medical M. R., Book M. A. Butler H. C., Marrell 19. B. Detter A., Change S.G., Schert S.E., ILP 78. Hoskits R.A., Galle R.F.,
Ray Marrell 19. G., Wortman J.R., Tannoll I. Waster L.M., G., Marrell 19. B., Marrell 19. R.A., Bencon R.A., Hondy S., Dahy M., Marrell 28. G., Marrell 28. G., Marrell 29. B., Marrell 29. Marrell 29.
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EMBL; X14112; CAA32318.1;
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PROPEP
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                                                                                                                                                                       SITE
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                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Capsid protein P40 (Virion structural protein UL26) [Contains: Capsid
Protein VP24 (Assemblin) (Protease) (EC 3.4.21.97); Capsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=88274327; PubMed=2839594;

MGGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,

MGGeoch D.J., Scott J.E., Taylor P.;

"The complete DNA sequence of the long unique region in the genome of herpes simplex virus type 1.";

J. Gen. Virol. 69:1531-1574(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Davison M.D., Rixon F.J., Davison A.J.;
"Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes simplex virus type 1.";
of herpes simplex virus type 1.";
J. Gen. Virol. 73:2709-2713(1992)
- FUNCTION: VP22A IS A COMPONENT OF THE CAPSID CORE INVOLVED IN PROCESSING AND PACKAGING OF PROGENY DNA. VP24 IS A PROTEASE WHICH CAN PROTEOLYTICALLY CLEAVE ITSELF AND VP22A AT THE C-
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Preferentially cleaves at Ala-|-Ser or Ala-|-
                                                                                                                                                                                                                        ô
 Repeat.
7 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO PEPTIDASE FAMILY S21.
SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP40
                                                                                                                                                                                             Score 47; DB 1; Length 463; Pred. No. 24;
                                                                                                                POLY-PRO.
H-T-H MOTIF (POTENTIAL).
PM -> HH (IN REF. 1).
GGPPP -> VDHHR (IN REF. 1).
D03C097192D1FDD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herpes simplex virus (type 1 / strain 17).
Vituses; dsDNA viruses, no RNA stage; Herpesviridae;
Apphaherpesvirinae; Simplexvirus.
NCBI_TaxID=10299;
                                                                                                                                                                                                                                                                                                                                        635 AA
                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 11-29; 77-91 AND 223-241.
                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: VP22A IS PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                               01-MAR-1989 (Rel. 10, Created)
                                                                                                                                                                     MM;
                                                                                                                                                                                          62.7%;
                                                                                                                                                                                                         70.08;
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                                                                                                                                                                     51267
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                       STANDARD;
 Nuclear
                                                                                                                                                    282
463 AA;
                                                                                                                                                                                                                                                                      278 MGPMGGPPPP 287
                                                                                                                                                                                                        Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                              2 LGPQGRPPPP 11
              87
87
95
110
111
127
127
284
3397
DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TERMINUS
                                                                                                                                                                                                                                                                                                                                      VP40_HSV11
P10210;
                                                                                                              DOMAIN
DNA_BIND
CONFLICT
                                                                                                                                                    CONFLICT
                                                                                                                                                                                             Query Match
                        REPEAT
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REPEAT
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                               VP22A].
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                                                                                                                                                                                                                   Matches
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CAPSID PROTEIN VP24.
CAPSID PROTEIN VP22A.
C-TERMINAL PEPTIDE.
CLEAVAGE (BY THE PROTEASE) (PROBABLE).
CLEAVAGE (BY THE PROTEASE) (PROBABLE).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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-!- SIMILARITY: BELONGS TO THE FIBRILLAR CLASS OF COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rowen L., Qin S., Madan A., Loretz C., James R., Dors M., Mix L.,
Hall J., Lasky S., Hood L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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                                                                                                                                                                        Coat protein; Hydrolase; Serine protease; Phosphorylation. CHAIN 1635 GENE UL26 PROTEIN. CHAIN 253 635 GENE UL26.5 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F3B3C7D42F3D062D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           064739; 0921W0;
15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Collagen alpha 2(XI) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1650 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                       MEROPS; S21.001; -: InterPro; IRR001847; Assemblin. Pfan: PF00716; Peptidase_S21; 1. PRINTS; PR00236; HSVCAPSIDP40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66470 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.78;
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nes 7; Conservative
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129
148
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247
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611
PIR; H30084; WMBEW6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      635 AA;
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565 PPGPPPPC 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=129/SvJ;
                                 HSSP; P16753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA2B_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                 ACT_SITE
ACT_SITE
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SEQUENCE
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SECUENCE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The human COL11A2 gene structure indicates that the gene has not
                                                                                                                                                                                                                                                                                                                                                                               Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Alternative splicing; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         evolved with the genes for the major fibrillar collagens.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOXYL-TERMINAL PROPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        • M (IN REF. 2).
8ECDB8702E71E2DA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA2B_HUWAN STANDARD; PRT; 1736 AA. P13942; Q13273; Q13271; Q13272; Q07751; Q99866; Q9UIP9; Q1-JAN-1990 (Rel. 13, Created) 16-OCN-1990 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NONHELICAL REGION.

R -> L (IN REF. 2).

NQ -> KP (IN REF. 2).

V -> A (IN REF. 2).

TGP -> HGS (IN REF. 2).
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TRIPLE-HELICAL REGION.
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Pred. No.
                                                                                                                                 MGD; MGI:88447; COIl1a2.
InterPro; IPR000087; COllagen.
InterPro; IPR001089; Ftb_collagen_C.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR001230; TSPN.
Pfam; PF01391; Collagen; I8.
Pfam; PF01310; COLFF; 1.
Pfam; PF02101; TSPN: 1.
ProDom; PD000007; Collagen; 4.
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                                                                                      EMBL; AF100956; AAC69905.1; -.
EMBL; U16789; AAA67751.1; -.
EMBL; U16790; AAA67752.1; -.
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80.0%;
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SM00210; TSPN; 1
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Best Local Similarity
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Matches
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Zhidkova N.I., Brewton R.G., Mayne R.; "Molecular cloning of PARP (proline/arginine-rich protein) from human cartilage and subsequent demonstration that PARP is a fragment of the NH2-terminal domain of the collagen alpha 2(XI) chain."; FEBS Lett. 326:25-28(1993).
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MEDLINE-893404085; Pubmed=2760050;
Kimura T., Cheah K.S.E., Chan S.D.H., Lui V.C.H., Mattei M.-G.,
Van der Rest M., Ono K., Solomon E., Ninomiya Y., Olsen B.R.;
"The human alpha 2(XI) collagen (COLILA2) chain. Molecular cloning of
CDNA and genomic DNA reveals characteristics of a fibrillar collagen
With differences in genomic organization.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lui V.C., Ng L.J., Sat E.W., Cheah K.S.;
"The human alpha 2(XI) collagen gene (COL11A2): completion of coding information, identification of the promoter sequence, and precise localization within the major histocompatibility complex reveal Genomics 32:401-412(1996).
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MEDLINE=95163096; PubMed=7859284;

MEDLINE=95163096; PubMed=7859284;

Wikula M., Mariman B.C.M., Lui V.C.H., Zhidkova N.I., Tiller G.E., Goldring M.B., van Beersum S.E.C., de Waal Malefljt M.C., van den Hoogen F.H.J., Ropers H.-H., Mayne R., Cheah K.S.E., Olsen B.R., Warman M.L., Brunner H.G.,

"Autosomal dominant and recessive osteochondrodysplasias associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koga H., Sakou T., Taketomi E., Hayashi K., Numasawa T., Harata S., Yone K., Matsunaga S., Otterud B., Inoue I., Leppert M.; "Genetic mapping of ossification of the posterior longitudinal ligament of the spine.";
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MEDLINE-95238468; PubMed-7721876;
Shidkova N.I., Justice S.K., Mayne R.;
"Alternative mRNA processing occurs in the variable region of the pro-alpha 1(XI) and pro-alpha 2(XI) collagen chains.";
J. Biol. Chem. 270:9486-9493(1995).
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                                                                                                                                                             Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
J. Biol. Chem. 270:22873-22881(1995).
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                                                                                                                                                                                                                                                                                                    TISSUE=Cartilage;
MEDLINE=93314796; PubMed=8325374;
                                                                                                                                                                                                                                                       59-807 FROM N.A.
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                                                                                     SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Huntingtin (Huntington's disease protein homolog) (HD protein).
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Hameister H., Epplen J.T., Riess O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1736;
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ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; CoLFI; 1.
SMART; SM00282; LamG; 1.
SMART; SM00210; TSPN; 1.
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Interpro; IPR000885; Fib_collagen_C.
Interpro; IPR001791; Laminin_G.
Interpro; IPR001230; Prenyl_site.
Interpro; IPR001230; Prenyl_site.
                                                                                                                                                                                                            EMBL, U32169, AAC50214.1; -
EMBL, U32169, AAC50213.1; -
EMBL, U32169, AAC50215.1; -
EMBL, AL031228; CAA20240.1; -
EMBL, AL031228; CAA20240.1; -
EMBL, U4069, AAA17464.1; -
EMBL, U41069, AAC17464.1; -
EMBL, U41066; AAC17464.1; JOINED.
EMBL, U41066; AAC17464.1; JOINED.
EMBL, U41067; AAC17464.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01391; Collagen; 18.
Pfam; PF01410; COLFI; 1.
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MIM; 215150; -.
MIM; 277610; -.
MIM; 601868; -.
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P51111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 during
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
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       δλ
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Zweymueller syndrome (WZS), an autosomal dominant disorder allelic with STL3 and OSMED. It is also referred to as heteroxygous OSMED. DISEASE: Defects in COLILA2 are the cause of autosomal dominant
                                                                                                  PubMed=9805126;
Pihlajamaa T., Prockop D.J., Faber J., Winterpacht A., Zabel B.,
Giedion A., Wiesbauer P., Spranger J., Ala-Kokko L.;
"Heterozygous glycine substitution in the Coll1A2 gene in the original
patient with the Weissenbacher-Zweymueller syndrome demonstrates its
identity with heterozygous GNMED (nonocular Stickler syndrome).";
Am. J. Med. Genet. 80:115-120(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMOUNTS.

DISEASE: Defects in COL11A2 are the cause of Stickler syndrome type 3 (STL3). It is an autosomal dominant disorder characterized by oro-facial, auditory and skeletal manifestations, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           midfacial hypoplasia, cleft palate, osteoarthritis, and sensorineural hearing loss. Differently from Stickler syndrome type 1 and 2, no ocular involvement is observed. This disorder is also referred to as Stickler-like syndrome or non-ocular Stickler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONTROLLING LATERAL GROWTH OF COLLAGEN II FIBRILS.
SUBUNIT: TRIMERS COMPOSED OF THREE DIFFERENT CHAINS: ALPHA 1(XI),
ALPHA 2(XI), MND ALPHA 3(XI), ALPHA 3(XI) IS A POST-TRANSLATIONAL
MODIFICATION OF ALPHA 1(II). ALPHA 1(Y) CAN ALSO BE FOUND INSTEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sirko-Osadsa D.A., Murray M.A., Scott J.A., Lavery M.A., Warman M.L., Robin N.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF ALPHA 3(XI)=1(II).

ALTERNATIVE PRODUCTS: 8 isoforms; 1 (shown here), 2, 3, 4, 5, 6, and 8: way be produced by alternative splicing. They lack exons 6 7 or 8 or a combination of these exons. PTM: PROLINES AT THE THIRD POSITION OF THE THEEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. PTM: A DISULEIDE-BONDED PEPTIDE CALLED PROLINE/ARGININE-RICH PROTEIN OR PARP IS RELEASED FROM THE AMINOT TERMINISTING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nonsyndromic sensorineural deafness type 13 (DFNA13). Affected individuals experience progressive hearing loss beginning in the second to fourth decades, eventually making use of amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Stickler syndrome without eye involvement is caused by mutations in COL11A2, the gene encoding the alpha-2(XI) chain of type XI collagen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS DFNA13 GLU-808 AND CYS-1034, AND REVISIONS TO 1031-1032. MEDLINE-20047768; PubMed-10581026; McGuirt W.T., Prasad S.D., Griffith A.J., Kunst H.P.M., Green G.E., Shpargel K.B., Runge C., Huybrechts C., Mueller R.F., Lynch E., King M.-C., Brunner H.G., Cremers C.W.R.J., Takanosu M., Li S.-W., Arita M., Mayne R., Prockop D.J., Van Camp G., Smith R.J.H.; Matations in Collla2 cause non-syndromic hearing loss (DFNA13)."; Nat. Genet. 23:413-419(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR PROCESSING AND IS SUBSEQUENTLY RETAINED IN THE CARTILAGE MATRIX FROM WHICH IT CAN BE ISOLATED IN SIGNIFICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASS OF COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WWW="http://www.uia.ac.be/dnalab/hhh/hhhgenes.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DATABASE: NAME=Hereditary hearing loss homepage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE FIBRILLAR
J. Hum. Genet. 62:1460-1467(1998)
                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT STL3 940-GLY--PRO-948 DEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pediatr. 132:368-371(1998).
                                                                       VARIANT WZS GLU-955.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=9506662;
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Gaps

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Rommens J.M., Hayden M.R.;
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                                                                    VESICLE FUNCTION:

-1-SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
-1-SUBCELLULAR LOCATION: CYTOPLAR AND IN ALIGHER FEGIONS
-1-SUBCHERARY MOUSCLE, LIVER, LOW AND KIDREY.
-1-BURGUES HEART, MOUSCLE, LIVER, LOWA AND KIDREY.
-1-BURGUES AS EARLY AS DAY 14.5. THIS EXPRESSION REMAINS CONSTANT
IN ALL FURTHER DEPENDARY STAGES (UP TO THE ADULT). ON THE OTHER
HAND THE EXPRESSION IN MOUN NEURONAL TISSUES IS DOWN-REGULATED FROM
STAGE 17.5 DAY OLD EMBRYOS.
Strong T.V., Tagle D.A., Valdes J.M., Elmer L.W., Boehm K., Swarcop M., Kaatz K.W., Collins F.S., Albin R.L.; "Widespread expression of the human and rat Huntington's disease gene in brain and nonneural tissues.";
                                                                                                                                                                                                          -!- POLYMORPHISM: THE POLY-GLN REGION DOES NOT APPEAR TO BE POLYMORPHIC, EXPELINING THE ABSENCE OF A RODENT HD-LIKE DISORDER.
-!- SIMILARITY: CONTAINS 10 HEAT REPEATS.
-!- SIMILARITY: BELONGS TO THE HUNGTINTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                              Nat. Genet. 5:259-265(1993).
-!- FUNCTION: MAY PLAY A ROLE IN MICROTUBULE-MEDIATED TRANSPORT OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Huntingtin (Huntington's disease protein homolog) (HD protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
STRAIN=C57BL/6; TISSUE=Brain, and Spleen;
MEDLINE=94214482; PubMed=8162057;
Lin B., Nasir J., Macdonald H., Hutchinson G., Graham R.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 1; Length 3110;
Pred. No. 1.4e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33C357E8FC141550 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEATS DOMAIN 1.
REPEATS DOMAIN 2.
REPEATS DOMAIN 3.
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POLY-GLN.
POLY-PRO.
POLY-PRO.
POLY-THR.
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EMBL; U01022; AAC52133.1; -.
InterPro; IPR000091; Huntingtin.
Pfam; PF03541; Huntingtin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF03541; Huntingtin; 1.
PRINTS; PR00375; HUNTINGTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.7%;
87.5%;
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Best Local Similarity 87.55
France 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            297
911
1544
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38
51
1411
2611
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38 PQGQPPPP 45
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1408
2606
3110
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P42859;
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- 1- SUBCELLULAR LOCATION:
- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a short form; seem to be produced by alternative splicing. The short form; cannot be explained by a simple splicing. The short form cannot be explained by a simple splicing. The short form cannot be explained by a simple splicing. The short form cannot be explained by a simple splicing. The BRAIN, BUT IT IS ALSO FOUND IN THE STOWACH, HEART, TESTIS, ADIPOSE TISSUE, MUSCLE, SPREEN LIVER, AND KIDNEY.
- DEVELOPMENTAL STAGES. IN 14.5 DAY OLD EMBRYOS, IT IS ALSO DETECTED IN NON-NEURONAL TISSUES. THIS EXPRESSION IS DOWN-RECURANDED IN LATER STAGES OF DEVELOPMENT.
- POLYMORPHISM: THE FIRST POLY-PRO REPEAT STRETCH DIFFERS IN LENGTH BY ONE UNIT (THREE) IN MUS SPRETUS STRAIN COMPARED TO OTHER STRAINS (FORR). THE POLY-GLN REGION DOES NOT APPEAR TO BE POLYMORPHIC, EXPLAINING THE ABSENCE OF A MURINE HD-LIKE DISORDER.
- STRAILARAITY: CONTAINS 10 HEAT REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                     conservation, alternate splicing and polymorphism in a triplet (CCG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goldberg Y.P., Hayden M.R.; "Structural analysis of the 5' region of mouse and human Huntington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease genes reveals conservation of putative promoter region and di- and trinucleotide polymorphisms."; Genomics 25:707-715(1995).

-!- FUNCTION: MAY PLAY A ROLE IN MICROTUBULE-MEDIATED TRANSPORT OR VESICLE FUNCTION.
                                                                                                                                                                                                                                                      Barnes G.T., Duyao M.P., Ambrose C.M., McNeil S., Persichetti F., Srinidhi J., Gusella J.F., Macdonald M.E.; "Mouse Huntington's disease gene homolog (Hdh)."; Somat. Cell Mol. Genet. 20:87-97(1994).
                                                                                                                                                                                                                                                                                                                                                                                                   (3)
SEQUENCE FROM N.A.
MEDLINE-95375771; PubMed=7647777;
Trottier Y., Devys D., Imbert G., Saudou F., An I., Lutz Y.,
Weber C., Agid Y., Hirseh B.C., Mandel J.L.;
"Cellular localization of the Huntington's disease protein and
discrimination of the normal and mutated form.";
Nat. Genet. 10:104-110(1995).
Sequence of the murine Huntington disease gene: evidence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin B., Nasir J., Kalchman M.A., McDonald H., Zeisler J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----
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Alternative splicing; Polymorphism; Repeat.
noMAIN 182 306 HEAT REPEATS D
TOWN TRPEATS D
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                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-94278649; Pubmed-8009370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000091; Huntingtin.
                                                                                                      Hum. Mol. Genet. 3:85-92(1994).
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                                                                           repeat.
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                                                                                                                                                                                    Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Rawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura Y., Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

-- SUBUNIT: Interacts with topoisomerase 1.

-- TISSUE SPECIFICITY: Ubiquitous; higher levels in heart and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                    s.
                                                                                       Ω.
                             Withmann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D Wambutt R., Korn B., Klein M., Poustka A.; Tampe J., Heubner D "Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 1; Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           525A49E01728AFF0 CRC64;
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C -> G (IN REF. 2).
L -> P (IN REF. 4).
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                  skeletal muscle.
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TISSUE=Testis;
MEDLINE=21154917; PubMed=11230166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=BAISTON N2;
MEDINE=8925506; Pubmed=2498337;
Barstead R.J., Waterston R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL136853; CAB66787.1; -. EMBL; AF355402; AAK25825.1; -. EMBL; AF257241; AAK17068.1; -. EMBL; AK000731; BAA91345.1; -. Genew; HGNC:1120; BFBD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52771 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; newn.tack, ......
Fram; PF00651; BTB, 1.
SMART; SM0025; BTB; 1.
PROSITE; PS50097; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        482 AA;
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Matches 8; Conserv
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P19826;
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Yang L., Xu L., D'Arpa P.;
"Characterization of two similar BTB-containing Kelch-like proteins,
BTBD1 and BTBD2, identified as topoisomerase I-interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carim-Todd L., Sumoy L., Andreu N., Estivill X., Escarceller M.; identification and characterization of BTBD1, a novel BTB domain containing gene on human chromosome 15q24."; Gene 262:275-281(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW; ECA42B5916F50F4F CRC64;
                                                                                                                      SHORT ISOFORM).
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REPEATS DOMAIN 3.
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A -> P (IN REF. 1).
A -> P (IN REF. 1).
A -> P (IN REF. 1).
D -> E (IN REF. 1).
D -> E (IN REF. 1).
T -> N (IN REF. 1).
D -> G (IN REF. 1).
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SEQUENCE FROM N.A.
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     QΥ
                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF
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PROBOSCIPEDIA SUBFAMILY.
                                                                                                                               -!- SUBUNIT: EXHIBITS SELF-ASSOCIATION PROPERTIES.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC FACE OF ADHESION PLAQUES.
-!- SIMILARITY: STRONG, TO OTHER VINCULINS AND TO ALPHA-CATENINS.
"The basal component of the nematode dense-body is vinculin."; J. Biol. Chem. 264:10177-10185(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell adhesion; Actin-binding; Cytoskeleton; Structural protein; Phosphorylation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                             ATTACHMENT OF THE ACTIN-BASED MICROFILAMENTS TO THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46; DB 1; Length 1010;
Pred. No. 66;
3; Mismatches 3; Indels
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01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
HOMACODOX PICCEIN HOX-A2.
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MEDLINE-95324377; PubMed-7600967;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J04804; AAA28002.1; -.
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Matches 8; Conservative
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                                                                                                            MEMBRANE.
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypermethylated in cancer 2 protein (Hic-2) (Hic-3) (HIC1-related gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alliel P.M., Goudou D., Bitoun M., Seddigi N., Rieger F., Perin J.-P., "Complete deduced structure of HIC-3, a novel human btb/poz and ZF factor of the HIC family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Babbage A.K., Calamp M., Smink L.J., Alnscough R., Almeida J.P., Babbage A.K., Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J., Bridgeman A.M., Buck D., Burgess J., Carder C., Carter N.P., Chen Y., Clark G., Clegs S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deltour S., Pinte S., Guerardel C., Leprince D.; "Characterization of HRG22, a human homologue of the putative tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Macazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-85 FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING MEDLINE=21438979; PubMed=11554746;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homeobox; DNA-binding; Developmental protein; Nuclear protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C7C4CA10455C3B11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTP-TYPE HEXAPEPTIDE. HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       suppressor gene HIC1.";
Biochem. Biophys. Res. Commun. 287:427-434(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                               EMBL; X74323; CAA52370.1; -. HSSP; P14653; 1B72.
TRANSFAC; T01700; -. InterPro; IPR001827; Antennapedia. InterPro; IPR001825; Homeobox. Pfam; PP00046; homeobox: 1. PRINTS; PR00025; ANTENNAPEDIA. PRINTS; PR000024; HOMEOBOX. PRODOM: PD000010; Homeobox: 1.
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                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00389; HOX; 1.

PROSITE: PS00027; HOMEDBOX_1; 1.

PROSITE: PS50071; HOMEDBOX_2; 1.

PROSITE: PS00032; ANTENNAPEDIA; 1.
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77.8%;
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HIC2 OR HRG22 OR KIAA1020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation.
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Matches 7; Conservative
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Search completed: February 5, 2003, 09:48:19
Job time : 10.5714 secs
                       EMBL; AL162003; CAB82344.1;
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RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Garner A.A.,

Rad Gilbert J.G.R., Geward M. E., Grafham D.V., Griffiths M.N.D., Hall C.,

Rad Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,

Rad Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,

Rad Martyn I.D., Mashreqhi-Wohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Paritt R., Pearce A.V., Pearson D., Phillimore B.J.,

RA Mcclay J., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J.,

RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,

RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Scott U.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Scott U.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Scott C.E., Hubbard T., Bentley D.R., Beck S., Rodon J.,

RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

RA Milliams S.A., Williams C.A., Rodor J.,

RA Shintani A., Shibuya K., Yoshizaki Y., Asakawa S., Rodon J.,

RA Borman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,

RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Vao Z.,

RA Borman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Yao Z.,

RA Dorman A., Fang S., Lin S.-P., Loh P., Malaj E., Nuyen T., Pan H.,

RA Donnan S., Oi S., Oian Y., Ray L., Ren O., Shaull S., Sloan D., Song L.,

RA Hinds K., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,

RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,

RA Hinds K., Lanker C., Wamsley A., Wohldmann P., Pepin K., Milson P.,

Ranuell B.S., Shaikh T., Kurahashi H., Saltta S., Budarf M., Kedra D.,

Ranuell B.S., Shaikh T., Kurahashi H., Saltta S., Budarf M., Kedra D.,

Ranuell B.S., Shaikh T., Rurahashi H., Saltta S., Budarf M., Kedra D.,

Ranuell B.S., Shaikh T., Rurahashi H., Shikuya R., Ranuell R., Shizuya H., Shixuya H., Shixuya H., Shi
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Kikuno R., Nadase T., Ishlkawa K.-I., Hirosawa M., Miyajima N.,
Tranaka A., Kotani H., Nomura N., Obara O.;
"Prediction of the coding sequences of unidentified human genes. XIV.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 6:197-205(1999).
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-- SUBCELLULAR LOCATION: Nuclear.
-- ALTERNATURE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
-- TISSUE SPECIFICITY: Highest Levels in cerebellum.
-- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H9-TYPE ZINC-FINGER PROTEINS. HIC TRANSCRIPTION FACTORS SUBFAMILY.
-- SIMILARITY: CONTAINS 1 BTB/FOZ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koehrer K., Beyer A., Mewes H.-W., Weil B., Wiemann S., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases -: FUNCTION: Transcriptional repressor.
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AP000557; -; NOT_ANNOTATED_CDS. AB028943; BAA82972.1; -.

EMBL;

EMBL; AJ313204; CAC70715.1; -. AF349035; AAK72951.1; -. AP000557; -; NOT_ANNOTAT

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Gaps
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Genew; HGNC.18595; HIC2...
InterPro: IPR000210; BTB_POZ.
InterPro: IPR000322, Znf_C2H2.
Pfam; PF00051; BTB, 1.
Pfam; PF00056; Znf_C2H2; 5.
SMART; SM00355; Znf_C2H2; 5.
PROSITE; PS50097; BTB, 1.
PROSITE; PS50097; ZINC_FINGER_C2H2_1; 5.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.
DNA-binding; Zinc-finger; Metal-binding; Repressor;
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 615;
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615 ZINC FINGERS.
6469 CZH2-TYPE.
532 CZH2-TYPE.
560 CZH2-TYPE.
615 CZH2-TYPE.
615 CZH2-TYPE.
615 CZH2-TYPE.
71 BINDING TO CTBP.
71 IN -> TIT (IN REF. 1).
71 IN -> TR (IN REF. 1).
71 IN -> TR (IN REF. 1).
71 G6155 MW; B0368C631B198C95 CRC64;
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0; Mismatches
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les 7; Conservative
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246
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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SPTREMBL_21:*

1. sp_archea:*
2. sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_manmal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_blage:*
10: sp_plage:*
11: sp_virus:*
12: sp_virus:*
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               671580 seqs, 206047115 residues
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75
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Copyright (c) 1993 - 2003 Compugen Ltd.
sp_vertebrate:*
sp_unclassified:*
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sp_archeap:*
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sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

16	15	14	13	12		10	9	. &	7	ا م	. <b>G</b>	.4	· tu	· N.	, 1		Result	
46	46	47	47	4.7	47	47	48	4.8	48	4.8	49	49	50	51	51	Score		
61.3	61.3	62.7	62.7	62.7	62.7	62.7	64.0	64.0	64.0	64.0	65.3	65.3	66.7	68.0	68.0	Match	Query	æ
139	112	1827	635	333	329	67	1616	373	327	211	2241	858	411	297	261	Match Length		
11	17	13	12	16	12	1	4	4	IJ	Ŋ	υı	13	16	11	10	DB		
Q9CTN9	Q9YEB0	Q8UUM5	Q69087	Q9L009	009798	Q9Z1I8	015054	Q9NP08	001799	045098	015850	Q8UVX0	Q9FCM3	Q9JLV7	Q9CAE4	ID		Commission
_	aeropyru				009798 human herpe	Q9z1i8 rattus norv	015054 homo sapien	Q9np08 homo sapien	001799 caenorhabdi	O45098 caenorhabdi	O15850 leishmania			Q9jlv7 mus musculu	Q9cae4 arabidopsis	Description		120

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
44	44	44	44	44	44	44	44	44	44	45	45	45	45	45	45	45	45	45	45	45	46	46	46	46	46	46	46	46
58.7	•	•	•	•	•	•	•				•	•	•	•	•		•	•	•				•	•	•	61.3		
329	309	297	243	238	176	173	142	142	85	1820	1184	756	705	533	533	432	388	363	363	253	1784	1500	1014	993	. 579	502	373	230
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Q17166	Q04118	Q16038	Q9F1Q4	000600	Q9C4Z8	Q15214	Q8R5H4	Q8VCS6	070555	Q9I907	Q9V5D2	P72877	Q8TEJ5	Q9STK1	Q8VYS5	Q21414	Q96Н72	Q94C63	Q9ZU66	Q9VMF9	Q8S5L6	Q94DA0	Q9BI32	Q9VY31	Q9LGG8	Q8S5L3	Q9BI31	Q9W3V7
brug	homo	Q16038 homo sapien	ther	5	3 arab		mus	mus	070555 mus musculu	$\sim$	drosophila	P72877 synechocyst			S							Q94da0 oryza sativ	Q9bi32 caenorhabdi	irosopi	oryza	w		Q9w3v7 drosophila

## ALIGNMENTS

9CAE4 9CAE4 9CAE4; 1-JUN-2001 (TrEMBLrel. 17, Created) 1-JUN-2001 (TrEMBLrel. 17, Last sequence update) 1-JUN-2001 (TrEMBLrel. 21, Last annotation update) 1-JUN-2002 (TrEMBLrel. 21, Last sequence update) 1-JUN-2002 (TrEMBLrel. 21, Last sequence) 1-JUN-2002 (TrEMBLrel. 21, Last sequence) 1-JUN-2002 (TrEMBLrel. 21, Last sequence) 1-JUN-2002 (TrEMBLrel. 21, Sequence) 1-JUN-2002 (TrEMBLrel. 21, Last sequence 1-JUN-2002 (Trembedel 21, Last se	RA RA RA	RA RA	RA RA	RA RA RA	RR	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	Q9CAE4
RELIMINARY; PRT; 261 AA.  TERMBLrel. 17, Created) TERMBLrel. 17, Last sequence update) TERMBLrel. 21, Last sequence update) TERMBLrel. 21, Last sequence update) 29.4 kDa protein.  haliana (Mouse-ear cress). ridiplantae; Streptophyta; Embryophyta; Tracheo; Magnollophyta; eudicotyledons; core eudicots; Magnollophyta; eudicotyledons; core eudicots; Magnollophyta; Brassicaceae; Arabidopsis.  (N.A. LUMBIA; 720; Pubbed=11130713; 720; Pubbed=11130713; 720; Pubbed=111.A., Mache R., Puigdomenceb Choisne N., Artiguenave F., Robert C., Borettie attolico L., Weissenbach J., Saurin W., Quetter Wueller-Auer S., Gabel C., Fuchs M., Benes V., Drzonek H., Erfle H., Jordan N., Bangert S. V., Caranek H., Schoen O., Bargues M., Terol J., Cl Dilado C., Perez-Perez A., Ottenwaelder B., Nasuy D., Rranfe M., Schoen O., Bargues M., Terol J., Cl Oilado C., Perez-Perez A., Ottenwaelder B., Masuy D., Barse A. C., Alcaraz JP., Cottet A., Casacuber rgiriou A., Flores M., Liguori R., Vitale D., Walls S., Town C.D., Koo H.L., Tallon L.J., Jen zon M., Walts A., Utterback T., Fujii C.Y., She Haas B., Maiti R., Wu D., Peterson J., Van Akmash S., Maiti R., Wu D., Peterson J., Van kon Scher J., Sellers P., Gill J.E., Feldblyum T.V. van X., Nierman W.C., Salzberg S.L., White O., Ve	Mayer K.F.X., Rooney T., Ri Creasy T.H., Pai G., Milit Preuss D., Li	de Haan M., M Monfort A., A Mannhaupt G.,	Wiedermann K. Vezzi A., D'A Conrad A., Ho Reichelt J., Navarro P., C	Delseny M., B De Simone V., Wincker P., C Schaefer M., Wurmbach E.,	(1) SEQUENCE FROM STRAIN=CV. CO MEDLINE=21016 Salanoubat M. Fartmann B.,	Hypothetical F13M14.33. F13m14.33. Arabidopsis t Eukaryota; Vi Spermatophyta eurosids II;	9CAE4 9CAE4; 1-JUN-2001 1-JUN-2001 1-JUN-2002
PRT; 261 AA.  Created) Last sequence update) Last annotation update) Last sequence update) Last annotation update) Last sequence update) Last sequence update) Last sequence update Last sequence Last seque	Kaul S., Town zzo M., Walts A Haas B., Maiti scher J., Selle n X., Nierman W	aarse A.C., Alc rgiriou A., Flo Haase D., Scho	, Kranz H., Vos ngelo M., Palla rnischer K., Ka Scharfe M., Sch Ollado C., Pere	Outry M., Grive Choisne N., Al attolico L., We Mueller-Auer S. Drzonek H., Eri	U.A. LUMBIA; 720; PubMed=11; 720; PubMed=11; Valle G., Bloec	29.4 kDa prote: haliana (Mouse: ridiplantae; St; Magnoliophyta Brassicales; Br	RELIMINARY; TrEMBLrel. 17, TrEMBLrel. 17, TrEMBLrel. 21,
AA.  AA.  AA.  a update)  ion update  ion update)  ion up	C.D., KOO H.I 1., Utterback R., Wu D., Pe ers P., Gill C	Daraz JP., ( Daraz JP., ( Dres M., Liguo Dof H., Rudd S	avicini A., To avicini A., To aver G., Loehr noen O., Bargu ez-Perez A., C	ell L.A., Macirtiguenave F., eissenbach J., eissenbach C., F., Gabel C., File H., Jordar	130713; ieger M., Anso	inear cress). treptophyta; I s; eudicotylec rassicaceae; I	PR Crea Last
	T., Tallon L.J., Jen T., Fujii C.Y., She terson J., Van Aken LE., Feldblyum T.V.	ottet A., Casacuber ori R., Vitale D., S., Zaccaria P., Mew			rge W., Unseld M., rAlonso M., Obermai	mbryophyta; Tracheo lons; core eudicots;	AA update) . update)

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Best Local
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MGD; MGI:1342772; K1f2.

InterPro; IPR002965; P_rich_extensn.

InterPro; IPR0002962; Znf_C2H2.

Pfam; PF00096; Zf-C2H2; 1.

PRINTS; PR01211; PRICHEXTENSN.

SMART; SW00355; ZnF_C2H2; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_2; 1.

DNA-Dinding; Metal-Dinding; Zinc-finger.

NON_TER

297

297

SEQUENCE

297 AA; 30812 MW; 4DF288DELFF
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InterPro; IPRO01878; Znf_CCHC.
Pfam; PF00076; rrm; 1.
Pfam; PF00098; zf-CCHC; 1.
SMARP; SM00360; RRM; 1.
SMART; SM00343; ZnF_C2HC; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS50102; RRM_RNP_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9JLV7;
Q1-OCT-2000 (TrEMBLrel. 15, C
Q1-OCT-2000 (TrEMBLrel. 15, L
Q1-JUN-2002 (TrEMBLrel. 21, L
Lung kruppel-like factor (Fra
KLF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser C.M., Kaneko T., Nakamura I., Saco V., Sasamoto S., Kimura T., Idesawa K., Kawashima I Kiyokawa C., Kohara M., Matsunoto M., Matsuno Nakayama S., Nakazaki N., Shinpo S., Takauchi Watanabe A., Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence and analysis of thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
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EMBL; AC011560; AAG51392.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         and upstream regulatory elements."; Gene 236:185-195(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schrick J.J., Hughes M.J., Anderson K.P., Croyle M.L., L: "Characterization of the lung Kruppel-like transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99365315; PubMed-10433980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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160 GPAGRPPPP 168
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                                          GPQGRPPPP 11
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261 AA; 2
                                                                                          Conservative
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88.9%;
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72.7%;
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Last annotation update)
                                                                                       Score 51; DB 1 Pred. No. 4.3; 0; Mismatches
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, Muraki A.,
, Wada T.,
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RESULT 4
Q8UVX0
ID Q8UV
AC Q8UV
DT 01-M
DT 01-M
DT 01-J
DE Piwi
OS Brac
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Best Local
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Q9FCM3;
Q1-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                          NON_TER
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Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacterida
Bacteria; Firmicutes; Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)."; coelicolor A3(2)."; Nature 417:141-147(2002).
EMBL; AL391454; CACC04103.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M. Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M. Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Cronin A., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=A3(2);
Bentley S.D., Parkhill J., I
Submitted (AUG-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative secreted oxidoreductase (Fragment). SCO7791A OR SC10B8A.01C.
                                                                                                                                                                                                                                                                               Pfam; PF01360; Monooxygenase; PRINTS; PR00420; RNGMNOXGNASE
                                                                                                                                                                                                                                                                                                                                                                                                       Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Microbiol. [4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaite D.,
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                                                                                                                                                GPQGRPPP
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8; Conser
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IPR003042; Rng_mnoxygenase.
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milarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                          44447 MW;
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e EMBL/GenBank/DDBJ databases
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Last
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Pred. No.
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8.1;
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hromosome.";
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Q8UVX0; Q8UVX0; 01-MAR-2002 01-MAR-2002 01-JUN-2002 Piwi protein

(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

20, 21,

Created)
Last sequence update)
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PRELIMINARY;

858

AA

Piwi protein. Brachydanio rerio (Zebrafish) (Zebra danio).

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RESULT
015850
ID 010 010
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Best Local
                   045098;
045098;
01-JUN-1998
01-JUN-1998
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myler P.J., Audleman L., deVos T., Hixson G., Kiser P. Myler B., S. Audleman E., Sisk E., Sunkin S., Swartzell Bastien P., Fu G., Ivens A., Stuart K.;

"Leishmania major Friedlin chromosome 1 has an unusua protein coding genes.";

Proc. Natl. Acad. Sci. U.S.A. 96:2902-2906(1999).

EMBL; AE001274; AAC24680.1; -.

InterPro; IPR000008; C2.

InterPro; IPR0000937; Viral_coat.
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"Cloning and characterization of zebrafish homolog of piwi, for germ-line stem cell self-renewal.";

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL: AF336369; AAL57170.1;

InterPro; IPR003100; PAZ.

InterPro; IPR003105; PAZ.

InterPro; IPR003155; Piwii.

Pfam; PF02170; PAZ; 1.

Pfam; PF02171; Piwii 1.

Pfam; PF02171; Piwii 1.
  Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00233; ICOSAHEDRAL.
SMART; SM00239; C2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
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01-NOV-1998
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NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                        Local
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8; Conservative
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2241 AA;
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(TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
L 24.1 kDa protein.
                                                                                                                                                                                                                                                                                                  Conservative
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A; 241669 MW;
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77.8%;
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Pred. No. 53;
1; Mismatches
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Matches 7
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01-JUL-1997 (
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Hypothetical
F53G12.7.
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Hypothetical protein.
SHOUENCE 211 AA; 2
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STRAIN-BRISTOL N2;
Bentley D., Le T.T.;
Bentley D., Le T.T.;
The sequence of C. elegans (100) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                              STRAIN-BRISTOL Waterston R.;
                                                                                                                                 Wu X., Graves T.;
"The sequence of C. of Submitted (MAY-1997)
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Rhabditidae; Pelode;
NCBI_TaxID=6239;
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ
EMBL; AF045644; AAC02599.1; -.
                       Waterston R.;
"Direct Submission.";
                                                                   SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                      None;
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MEDLINE=99069613; PubMed=9851916;
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(SEP-2001) to
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7 (TrEMBLrel. 04, 102)
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the EMBL/GenBank/DDBJ databases
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EMBL/GenBank/DDBJ
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Last annotation
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EMBL/GenBank/DDBJ databases.
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Pred. No.
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RESULT
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InterPro; IPR000087; Collagen.
InterPro; IPR002486; Col_cuticle_N.
Pfam; PF01391; Collagen; 2.
Pfam; PF01484; Col_cuticle_N; 1.
ProDom; PD000007; Collagen; 1.
Hypothetical protein.
SEQUENCE 327 AA; 33025 MW; 1DFACE
                                                                O15054; PRELIMINARY;
O15054; PRELIMINARY;
O1-JAN-1998 (TrEMBLrel. 05,
O1-JAN-1998 (TrEMBLrel. 05,
O1-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-binding; Homeow
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EMBL; M99587; AAF70205.1; -.
HSSP; P14653; 1B72.
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MEDLINE=93087572; PubMed=1360670;
MEDLINE=93087572; PubMed=1360670;
Stadler H.S., Padanilam B.J., Buetow K., Murray J.C
"Identification and genetic mapping of a homeobox go
region of human chromosome 4.";
Proc. Natl. Acad. Sci. U.S.A. 89:11579-11583(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2002 (TrEMBLrel. 20,
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InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH_repressr.
Pfam; PF00046; homeobox; 1.
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                        KIAA0346 protein (Fragment) KIAA0346.
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    Homo
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sapiens (Human).
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8; Conserv
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73 AA; 39225 MW; 8BF9EB1722660A76 CRC64;
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77.8%;
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Pred. No. 15;
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Pred. No. 13;
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RESULT 11
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                                                                                                                                    Query Match
Best Local S
Matches 7
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DNA Res. 4:141-150(1997).
EMBL; AB002344: PARATITE.
                                                                                                                                                                                                                                                                                                                                                                                          Q92118;
Q92118;
Q1-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-JUN-2001 (TrEMBLrel. 17,
009798 PRELIMINARY;
009798;
01-JUL-1997 (TrEMBLrel.
01-JUL-1997 (TrEMBLrel.
                                                                                                                                                                               NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                         "Isolation and characterization of t
Biochem. J. 336:227-234(1998).
EMBL; AJ224997; CAA12281.1; ".
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002965; P_rich_extensn.
InterPro; IPR003447; TF_JmjC.
InterPro; IPR001440; TPR.
InterPro; IPR001440; TPR.
Pfam; PF02373; JmjC; 1.
PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                           HOlzmann C., Maeueler W., Petersohn
Epplen J.T., Riess O.;
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                              4 PQGRPPPP 11
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                                                                                          PQGQPPPP
                                                                                                                                    Similarity 87.17; Conservative
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                                    PRELIMINARY;
                                                                                          53
                                                                                                                                                                                AA;
                                                                                                                                                                                7296 MW;
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70.0%;
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87.5%;
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Last annotation update)
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Pred. No.
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l; Mismatches
                                                                                                                                                         Score 47;
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                       Q9L009 PRELIMINARY; PRT; 333 AA.
Q9L009;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-UN-2002 (TrEMBLrel. 21, Last annotation update)
Putative dehydrogenase.
SCO2304 OR SCC30.12C.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; St
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human herpesvirus I.
"'rnses; dsDNA viruses, no RNA su
"'rnses; Simplexvirus.
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17.";
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UL26.
  STRAIN=A3(2);
Seeger K.J.,
                                         SEQUENCE FROM N.A.
                                                                                 NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00716; SEQUENCE 329
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InterPro; IPR001847; Assemblin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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Dolan A., McKie E.
"Status of the ICF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=86148504; PubMed=3005980; McGeoch D.J., Dolan A., Donald S., Brauer D.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=88274327; PubMed=2839594;
McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A.,
McNab D., Perry L.J., Scott J.E., Taylor P.;
"The complete DNA sequence of the long unique region i
herpes simplex virus type 1.";
j. Gen. Virol. 69:1531-1574(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=17
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К.J.,
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Harris
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AA; 33760
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ICP34.5 gene in herpes simplex v
                                                                                                     Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=1321882;
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14:1727-1745(1986)
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77.8%;
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                                                                                                Streptomycetaceae;
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STRAIN-A3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                 Q69087;
Q69087;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-94308117; PubMed-8034621;
Darke P.L., Chen E., Hall D.L., Sardana
Darke P.L., Shafer J.A., Kuo L.C.;
Lafemina R.L., Shafer J.A., Kuo L.C.;
            CHAIN
                                                                                                                                                                                                                                                        UL26.
                                    Pfam; P
PRINTS;
 SEQUENCE
                                                                                               J. Biol. Chem. EMBL; L32018; A
                                                                                                                                                                                                                  Viruses; dsDNA viruses,
Alphaherpesvirinae; Simp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL352972; CAB88182.1;
                                                             InterPro;
                                                                        MEROPS; S21.001;
                                                                                  HSSP; P16753;
                                                                                                                       Escherichia coli."
                                                                                                                              "Purification of active Herpes
                                                                                                                                                                                                       NCBI_TaxID=10298;
                                                                                                                                                                                                                                           human herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A set of ordered cosmids and a detaile
the 8 Mb Streptomyces coelicolor A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Redenbach M., Kieser H.M.
Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapaite
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Cerdeno A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the model actinomycete Streptomyces
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                                             Pro; IPR001847; Assemblin. Pr00716; Peptidase_S21; 1.
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8; Conserv
                                   PR00236; HSVCAPSIDP40
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             253
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                                                                                  1WPO.
                                                                                               AAA45828.1;
 AA;
                                                                                                         269:18708-18711(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
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             610
66454 MW;
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72.7%;
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19,
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e EMBL/GenBank/DDBJ databases.
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           HSV-1 PROTEASE
ICP35 ASSEMBLY
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3C7768EE1496FDBF CRC64;
                                                                                                                               simplex virus-1
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RESULT 15
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pfam; pF01410; CCLF; 1.

pfam; pF0210; TSPN; 1.

pfam; pF02210; TSPN; 1.

proDom; pD002078; Fib_ccllagen_C; 1.

smarr; sm00208; CCLF; 1.

smarr; sm00282; LamG; 1.

smarr; sm00210; TSPN; 1.

prOSITE; pS50025; LAM_G_DOMAIN; 1.

sequence 1827 AA; 181589 MW; AF
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01-MAR-2002
01-JUN-2002
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Beloniformes; Adrianichthyldae; Oryzias.
                                                                                                                                                                09YEB0;
01-NOV-1999 (TIEMBLIEL 12, C:
01-NOV-1999 (TIEMBLIEL 12, L:
01-MAR-2002 (TIEMBLIEL 20, L:
Hypothetical protein APE0864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenetics 0:0-0(2002).
EMBL; AB073376; BAB83839.1; -.
EMBL; AB073376; BAB83839.1; -.
InterPro; IPR000087; Collagen.
InterPro; IPR000885; Fib_collagen_C.
InterPro; IPR001791; Laminin_G.
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                                                                                       Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae; Aeropyrum.
                                                                                                                               Aeropyrum pernix.
                                                                                                                                                                                                                                                                                                Q9YEB0
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STRAIN-K1;
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Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., K Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Yakamura Y., Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Kl."; DNA Res. 6.83-101(1999).
                                                                                                                  EMBL; APRO00060; BAA79636.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 112 AA; 11931 MW; 9007CDD89321151E CRC64;
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Search completed: February 5, 2003, 09:49:16
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-08-446-692-73
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US-08-176-320-2
US-08-176-320-2
US-08-178-265-16
US-08-237-919-2
US-08-97-98-267-3
US-08-98-371B-12
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US-08-98-371B-12
US-08-98-371B-12
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US-08-98-371B-13
US-08-918-383-136-136
US-08-918-383-136-33
US-08-619-198-3
US-08-619-198-3
US-08-131-1205-4
US-08-188-223-6
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27, Appl
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20, Appl
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11 11	74.7%; ty 81.8%; ervative	llication US/08446692 510 TION: Anna and, Chang vi amb, Timothy NTION: Inmunogenic L NTION: and synthetic UENCES: 114 E ADDRESS: Maria C.H. Lin 5 Park Avenue YOTK  S -0053 ARBLE FORM: ARBLE FORM: Floppy disk IBM PC compatible YSTEM: PC-DOS/MS-DOS PATENTION PC-DOS/MS-DOS PATENTION DATA: NUMBER: US/08/446,6 ION: 424 TI INFORMATION: a C.H. Lin ACHEL STANGER: 29,323 OCKET NUMBER: 1151-4 TION INFORMATION: 1212/415-8745 516)751-6849 SEQ ID NO: 73: amino acids o acid o acid o acid o acid o acid o acid o acide c.H. DATA: ACTERISTICS: amino acids o acid o ac		1 4 4 4 6 4 4 6 4 4 6 6 6 6 6 6 7 1 1 4 4 6 6 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	Score 56; DB Pred. No. 0.0	692 etic L etic 51-4	ALIGNMENTS	US-08-478-546B-6 US-08-956-254-2 US-09-008-38B-1 US-09-015-815-1 US-09-15-815-1 US-08-188-223-4 US-08-968-466-4 US-08-478-546B-4 US-08-478-546B-4 PCT-US94-13205-5 US-09-281-766-19 US-09-281-766-19 US-08-680-9326-36 US-09-500-124-427 US-09-500-124-427 US-09-461-240-12 US-09-968-927-12
	1; 77; 1	HRH peptide const universal immune Version #1.25	VTS	254-8 254-2 2888-1 319-5 319-5 319-5 319-6 319-6 3203-4 4468-4 3205-5 3205-5 3205-5 3205-2 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-3 3205-
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                                                                                                 Sequence 2, Application US/08188223 Patent No. 5688506
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                                                                             GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Wang, Chang Yi
APPLICANT: Wang, Chang Yi
APPLICANT: Wang, Chang Yi
APPLICANT: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
   APPLICANT: Grimes, Stephen
APPLICANT: Scibienski, Robert
TITLE OF INVENTION: Immunogens
TITLE OF INVENTION: Releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
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APPLICATION NUMBER: US 08/229,275
FILING DATE: 14-APR-1994
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FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
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Local Similarity 81.8%;
les 9; Conservative
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amino acid
GY: linear
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345 Park Avenue
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(516)751-6849
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Immunogens Against Gonadotropin Releasing Hormone
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US-08-968-466-2
; Sequence 2, Application US/08968466
; Patent No. 6132720
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TELEPAX: 212-354-8113
TELEFAX: 212-354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
'ENGTH: 16 amino acids
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,223
FILING DATE: 27-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                   APPLICANT: Grimes, Stephen APPLICANT: Scibienski, Robert
COMPUTER READABLE FORM:
                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                       TITLE OF INVENTION: Immunogens Against TITLE OF INVENTION: Releasing Hormone
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CORRESPONDENCE ADDRESS:
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HYPOTHETICAL:
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STREET: 1155 Avenue of the Americas
CITY: New York
                          COUNTRY:
                                                            STREET: 1155 Av. CITY: New York
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                                                                            ADDRESSEE: DI
STREET: 1155
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SYSTEM: PC-DOS/MS-DOS
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                                                                                           Dimitrios T. Drivas, Esq
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                                                                            Avenue of the Americas
                                                                                                                                                        Immunogens Against Gonadotropin
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/note= "pyroglutamic acid (5-oxoproline)"
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MEDIUM TYPE:

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Best Local Similarity
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                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/0
FILING DATE: 27-JAN-1994
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NAME/KEY: Region
LOCATION: 1..10
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LENGTH: 16 amino acids
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REFERENCE/DOCKET NUMBER: 1102865-300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-819-8286
                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Grimes, Stephen APPLICANT: Scibienski, Rob
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LOCATION: 11..16
OTHER INFORMATION:
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CLASSIFICATION: 424
IOR APPLICATION DATA:
                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                 CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : peptide
YES
                                                                                                                                                                                                                                                                                                                     Tumors with Immunogens against Gonadotropin Releasing Hormone
                                                                                                                                                                                                                                                                                                                                          Methods for the Treatment of Hormone-Dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.0%; Score 48; DB 4; Length 16; 100.0%; Pred. No. 1.2;
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/note= "pyroglutamic acid (5-oxoproline)"
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                                                    US/08/478,546B
                                                                                                                                                                                                                                                                                                                                                         Robert
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US-07-832-855-2
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                 APPLICANT: ROIZHMAH, LIU, Fenyong
APPLICANT: Liu, Fenyong
TITLE OF INVENTION: Methods and Compositions of a
TITLE OF INVENTION: Preparation and Use of A Herpe
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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            REGISTRATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD045
TELECOMMUNICATION INFORMATION:
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                                                           ATTORNEY/AGENT INFORMATION: NAME: Coolley, Ronald B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                         FILING DATE: 1 CLASSIFICATION:
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                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                       ADDRESSEE: ARNOLD, WHITE & DURKEE STREET: 321 No. 5478727th Clark Street, Suite 800
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TELEPHONE:
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Pred. No.
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RESULT 8
US-08-457-273B-8
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US-08-176-320-2
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705
FIGURG DATE: 24 MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: COOLEY, Ronald B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)744-0090
INFORMATION FOR SEQ ID NO: 2:1
Sequence 8, Application Patent No. 5849995 GENERAL INFORMATION:
APPLICANT: Hayden, M
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Best Local S
Matches 7
                                                                                                                                                                         Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/176,320
                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS: Alice O. Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Liu, Fenyong
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: PREPARATION AND USE OF A HERPES !
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                                                                                                                 565 PPGPPPPPC 573
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                                                                                                                                             4 PQGRPPPPC 12
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ses 7; Conserv
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77.8%;
                                           US/08457273B
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Pred. No.
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Pred. No. 54;
                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                 DB 4; Length 635;
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CORPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION NUMBER: US/08/246,982A
APPLICATION NUMBER: US/08/246,982A
APPLICATION NUMBER: US/08/246,982A
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US-08-246-982A-16
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Matches 7
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Patent No. 5
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APPLICANT:
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TELEFAX: 919-854-1401
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MEDIUM TYPE: Floppy disk
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TOPOLOGY: lin
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1100 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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5686288
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Duyao, Mabel P.
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SYSTEM: PC-DOS/MS-DOS
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87.5%;
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Pred. No. 2.4e+02;
1; Mismatches C
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                                                        Matches
                                                                         Query Match
Best Local
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Best Local :
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                                                                                                                                                                                                      TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                               NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 060
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Duyao, Mader r.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
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REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3119 amino acids
                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/OFFILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
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les 7; Conserv
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                                                        Local Similarity es 7; Conserv
                                                                                                                                             TYPE: amino acid TOPOLOGY: linear
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PQGQPPPP 52
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1100 New York Avenue
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Duyao, Mabel P.
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ER: 29,021
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87.5%;
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                                                                      Score 47;
Pred. No.
                                                       Mismatches
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ches 0;
                                                                     2.4e+02;
                                                                                      DB 1;
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                                                                                   Length 3119;
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                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08732429 Patent No. 6300080 GENERAL INFORMATION:
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Matches 8; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks P.C
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: BO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R
REGISTRATION NUMBER: 36,6
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,919
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Wolf, Gre
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APPLICANT: Cepek, Karyn L
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TOPOLOGY:
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ZIP: 022
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CLASSIFICATION: 424
                                                                                             ZIP: 02210
                                                                                                         COUNTRY:
                                                                                                                                                   CITY:
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   SOFTWARE:
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PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                     Methods and Compositions for Modulating Heterotypic E-cadherin Interactions with T Lymphocytes
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

US/08/732,429

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RESULT 14
US-09-798-267-3
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Best Local Similarity
Whiches 8; Conservi
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                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-09-798-267-2
                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PARTY SEQ ID NO 2
LENGTH: 878
                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 2, Application US/09798267 Patent No. 6406870
                                                                    Sequence 3, Application US, Patent No. 6406870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Brenner, Michael
APPLICANT: Cepek, Karyn
TITLE OF INVENTION: Methods and Compositions for Modulating Heterotypic E-cadherin
TITLE OF INVENTION: Interactions with T Lymphocytes
FILE REFERENCE: L0560/7008ERP
CURRENT APPLICATION NUMBER: US/09/798,267
CURRENT FILING DATE: 2001-03-02
      APPLICANT: Brenner, Micl
APPLICANT: Cepek, Karyn
TITLE OF INVENTION: Me
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT
PRIOR FILING DATE: 1995-05-03
PRIOR APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 878 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 LGSQERSPPPC 29
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                                    Brenner, Micha
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Methods and Compositions for Modulating Heterotypic E-cadherin
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Best Local Similarity
Matches 8; Conserve
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                                                                   PCT-US95-05518-2
Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TYPE: PRT
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PRIOR FILING DATE: 1996-11-01
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 08/237,919
PRIOR FILING DATE: 1994-05-03
PRIOR APPLICATION NUMBER: PCT/US 95/05518
PRIOR FILING DATE: 1995-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/798,267
CURRENT FILING DATE: 2001-03-02
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                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   FILING DATE: herewith PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/2:
FILING DATE: 3 May 1994
ATTORNEY/AGENT INFORMATION.
                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks P.C
                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                       NAME: Plumer, Elizabeth R
REGISTRATION NUMBER: 36,6
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Search completed: February 5, 2003, 09:50:19
Job time : 15.1429 secs

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OM protein - protein search, using sw model
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Listing first 45 summaries
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Perfect score:
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          Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/U
2: /cgn2_6/ptodata/2/pubpaa/U
3: /cgn2_6/ptodata/2/pubpaa/U
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11: /cgn2_6/ptodata/2/pubpaa/U
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length: 2000000000
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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US-09-788-657-23	US-09-764-864-1261	US-09-764-864-800	US-09-957-995A-10	US-10-192-257-1	US-10-192-257-3	US-10-192-257-5	US-09-894-998-3	US-09-850-887-4	US-09-964-899-33	US-09-823-038A-33	US-10-001-887-137	US-09-905-831-21	US-09-919-497-56	US-10-001-887-108	US-09-905-983-48	US-10-165-049-3	US-10-165-049-2	US-10-192-257-2	ID	
		800	10,	Sequence 1, Appli	Sequence 3, Appli	, A	ω	Sequence 4, Appli	Sequence 33, Appl	Sequence 33, Appl	Sequence 137, App	21,	Sequence 56, Appl	Sequence 108, App	Sequence 48, Appl	Sequence 3, Appli	•	Sequence 2, Appli	Description	

#### ALIGNMENTS

RESULT 1 US-10-192-257-2

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RESULT 2
US-10-165-049-2
                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: MISC_FEATURE ; LOCATION: (1)...(1) ; LOCATION: (1)...(1) ; OTHER INFORMATION: Xaa=pyroglutamic acid US-10-192-257-2
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Best Local Similarity 80...
"Arches 8; Conservative
                                                                            Sequence 2, Application US/10165049 Publication No. US20020192724A1 GENERAL INFORMATION:
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Publication No. US20030021786A1
GENERAL INFORMATION:
APPLICANT: Aphton Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1 SEQ ID NO 2
APPLICANT: Brenner, Michael
APPLICANT: Cepek, Karyn
TITLE OF INVENTION: Methods and Compositions for Modulating Heterotypic E-cadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Condit TITLE OF INVENTION: Liver, Lung and Esophagus FILE REFERENCE: 1102865-0057 CURRENT APPLICATION NUMBER: US/10/192,257 CURRENT FILING DATE: 2002-07-09 PRIOR APPLICATION NUMBER: US 60/303,868 PRIOR EPILIAGION NUMBER: US 60/303,868 PRIOR FILING DATE: 2001-07-09
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PRIOR FILING DATE: 1994-05-03
PRIOR PPLICATION NUMBER: PCT/US 95/05518
PRIOR APPLICATION NUMBER: PCT/US 95/05518
PRIOR APPLICATION NUMBER: USSN 08/732,429
PRIOR APPLICATION NUMBER: USSN 08/732,429
PRIOR FILING DATE: 1996-11-01
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 9
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LENGTH: 878
TYPE: PRT
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 878
TYPE: PRT
                                                                                                 Query Match
Best Local
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                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Methods and Compositions for Modulating Heterotypic E-cadherin TITLE OF INVENTION: Interactions with T Lymphocytes FILE REFERENCE: L00560/70010ERP
                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1994-05-03
PRIOR APPLICATION NUMBER: PCT/US 95/05518
PRIOR FILING DATE: 1995-05-03
PRIOR APPLICATION NUMBER: USSN 08/732,429
PRIOR FILING DATE: 1996-11-01
PRIOR APPLICATION NUMBER: USSN 09/198,267
PRIOR FILING DATE: 2001-03-01
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CURRENT FILING DATE: 2002-06-07
CURRENT FILING DATE: 2002-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Brenner, Michael APPLICANT: Cepek, Karyn
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CURRENT FILING DATE: 2002-06-07
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LOCATION: (2225)..(2295)
OTHER INFORMATION: transmembrane
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LOCATION: (800)...(808)
OTHER_INFORMATION: HAV tripeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
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                                                                        Local Similarity es 8; Conserv
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  LGSQERSPPPC 29
                                      LGPQGRPPPPC 12
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                                                                            Conservative
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                                                                                            61.3%;
72.7%;
                                                                          Score 46; DB 97; Pred. No. 96; Mismatches
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"~+~hes 8; Conserve
                                                                                         RESULT 6
US-09-919-497-56
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-983-48
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                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapien US-10-001-887-108
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APPLICANT: Geiger, Benjamin
APPLICANT: Ben-Ze'ev, Avri
APPLICANT: Sadot, Einat
TITLE OF INVENTION: METHODS AND THERAPEUTIC COMPOSITIONS FOR TREATING CANCER
                                  Sequence 56, Application U Patent No. US20020106662A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Salceda, s
APPLICANT: Macina, H
APPLICANT: Recipon,
APPLICANT: Cafferkey
APPLICANT: Sun, Yong
APPLICANT: Liu, Cher
                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 108
LENGTH: 638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 108, Application US/10001887 Patent No. US20020155464A1
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CURRENT APPLICATION NUMBER: US/09/905,983
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/001,887 CURRENT FILING DATE: 2001-11-20 PRIOR APPLICATION NUMBER: 60/249,998 PRIOR FILING DATE: 2000-11-20 PRIOR APPLICATION NUMBER: 60/252,563 PRIOR FILING DATE: 2000-11-22
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes FILE REFERENCE: DEX-0269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1
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Sun, Yongming
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                                                                       Application US/09919497
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72.7%;
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72.7%;
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Pred. No.
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Pred. No.
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FILE REFERENCE: B0801/7225

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                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 21
LENGTH: 34
TYPE: PRT
              Sequence 137, Application US/10001887
Patent NO. US20020152464A1
GENERAL INFORMATION:
APPLICANT: SALceda, Susana
APPLICANT: Macina, Roberto
                                                                                                                                                                                                                                     Best Loc
Matches
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                                                                                                                                                                                                                                                                      Query Match
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Patent No. US20020119577a1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Best Local (
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NAME/KEY: UNSURE

LOCATION: (758)...(758)

OTHER INFORMATION: Xaa = NAME/KEY: UNSURE

LOCATION: (809)...(809)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/905,831
CURRENT FILLING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/276,313
PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/218,312
PRIOR FILING DATE: 2000-07-14 /
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zhang, Shuguang TITLE OF INVENTION: Direct, FILE REFERENCE: MLB-086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jacobson, Joseph APPLICANT: Schwartz, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: PXY34 peptide
                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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nes 7; Conserv
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Recipon, Herve
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Hamad, Kimberly
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Pred. No. 2.5e+02;
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8.5;
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                                                                                                                            ; Patent No. US20020174446A1 ; GENERAL INFORMATION:
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APPLICANT: Strachan, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Abernethy, Nevin
APPLICANT: Onrust, Rene
APPLICANT: Murison, Greg
APPLICANT: Murison, Greg
TITLE OF INVENTION: Compositions Isolated From Stromal Cells
FILE REFERENCE: 11000.1037c3
                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/823,038A CURRENT FILING DATE: 2001-07-09 NUMBER OF SEO ID NOS: 61
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 33
LENGTH: 322
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn version 3.1
SEQ ID NO 137
                                                                                                                                                                 Sequence 33,
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Best Local
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CURRENT APPLICATION NUMBER: US/09/964,899
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/236,893
                                                  APPLICANT: Cohen, Dalia et al.
TITLE OF INVENTION: Identification of Genes Involved in
TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
FILE REFERENCE: 4-31612 A
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CURRENT APPLICATION NUMBER: US/10/001,887

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 60/249,998

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: 60/252,563

PRIOR FILING DATE: 2000-11-22
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APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and
                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human
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                                                                                                                                                                Application US/09964899
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77.8%;
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Pred. No.
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PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2001-06-14

60/298,309

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                                                                                                                US-09-850-887-4
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US-09-850-887-4
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 1249
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09850887
Patent No. US20020009778A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 63.6%; Matches 7; Conservative
                                       Matches
                                                                           Query Match
                                                                                                                                                                                                                                                                                    NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0535
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          839 EIPPRRRPPPP 849
                                       Local Similarity nes 7; Conserv
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   3 GPQGRPPP 10
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FILING DATE: 07-May-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPDATIBLE
COMPUTER: FLOP PC COMPDATIBLE
COMPUTER: FOCDOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Word Perfect 6:1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/087,678 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOTGONE, GINA
TITLE OF INVENTION: THYROID AND PITUITARY MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 4
                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 4 :
                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                        LIBRARY: GenBank CLONE: g206712
                                                                                                                                                                                                                             LENGTH: 274 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: PALO ALTO
STATE: CALIFORNIA
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                                                                                                                                                                                                               TOPOLOGY: linear
                                       Conservative
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                                                         57.3%;
87.5%;
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Pred. No. 2.3e+02;
                                                         Score 43; DB Pred. No. 77;
                                       Mismatches
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RESULT 14
US-10-192-257-3
; Sequence 3, Application US/10192257
; Publication No. US20030021786A1
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANIEM: Herpes simplex virus
US-09-894-998-3
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US-10-192-257-5
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Best Local Similarity //...
Thes 7; Conservative
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Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Aphton Corporation
TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Condit
TITLE OF INVENTION: Liver, Lung and Esophagus
FILE REFERENCE: 1102865-0057
CURRENT APPLICATION NUMBER: US/10/192,257
CURRENT APPLICATION NUMBER: US/002-07-09
PRIOR APPLICATION NUMBER: US 60/303,868
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: McGowan, Patrick
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
FILE REFERENCE: 210121.538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/894,998
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 64
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                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 6
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                                                                                                                               1 RPPPPC
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Davin C. Dillon
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Pred. No.
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Pred. No. 2
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2.9e+02;
ches 2;
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; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; PAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa=pyroglutamic acid
US-10-192-257-1
                                                                                          Query Match
Best Local Similarity
"a+ches 6; Conserva
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Search completed: February 5, 2003, 09:56:02 Job time: 10.1429 secs
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US-10-192-257-1
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Publication No. US20030021786A1
GENERAL INFORMATION:
APPLICANT: Aphton Corporation
TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Condition
TITLE OF INVENTION: Liver, Lung and Esophagus
FILE REFERENCE: 1102865-0057
                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 56.0
Best Local Similarity 100
Matches 6; Conservative
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/192,257
CURRENT FILING DATE: 2002-07-09
PRIOR APPLICATION NUMBER: US 60/303,868
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 8
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4 RPPPPC 9
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                                                                              7 RPPPPC 12
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                                                                                                       56.0%; Score 42; DB 9; 100.0%; Pred. No. 5.8; tive 0; Mismatches
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100.0%; Pred. No. 1.1e+05;
tive 0; Mismatches 0;
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Minimum DB
Maximum DB
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length: 2000000000
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compus
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/cgn2_6/ptodata/1/paa/US085_COMB.pep:*
/cgn2_6/ptodata/1/paa/US086_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No. 1 2 3 4	Score 75 75 75	Query Match 100.0 100.0 100.0	Query Match Length DB ID 100.0 12 1 PC 100.0 12 1 PC 100.0 12 21 US 100.0 12 21 US	DB 1 1 21 21	DB ID    PCT-US99-10734-5   PCT-US99-10751-2   US-09-700-339-2   US-09-700-378-5	
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	75	100.0	12	21	US-09-700-329-2	
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σ	56	74.7	11	سإ	PCT-US94-04832A-73	
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### ALIGNMENTS

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RESULT 1
PCT-US99-10734-5

Sequence 5, Application PC/TUS9910734

GENERAL INFORMATION:
APPLICANT: Gevas, Philip C.
APPLICANT: Gevas, Philip C.
APPLICANT: Michaell, Dov.
APPLICANT: Method for the Treatment of Gastroesophageal Reflux
TITLE OF INVENTION: Disease
FILE REFERENCE: ACGIPCT
CURRENT FILING DATE: 1998-05-14
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: PCT/US99/10734
CURRENT FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 12
TYPE: PRT
ORGANISM: Unknown
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Description of Unknown Organism: human or
OTHER INFORMATION: synthetic peptide
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; LOCATION: (1)
; OTHER INFORMATION: pyroglutamic acid
PCT-US99-10751-2
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   Query Match
                                                                                                                                                      SEQ ID NO 2
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Gevas, Philip
APPLICANT: Grimes, Steph
APPLICANT: Karr, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Best Local Similarity 100.0%;
Matches 12; Conservative (
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                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US99/10751
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/085,714
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                APPLICANT: Watson, Susan TITLE OF INVENTION: Prevention and Treatment of Hypergastrinemia FILE REFERNCE: ACGUSA CURRENT APPLICATION NUMBER: US/09/700,329 CURRENT FILING DATE: 2001-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                             TYPE: PRT
ORGANISM: human gastrin peptide
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: pyroglutamic acid
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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ORGANISM: human or
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09700329
                                                                                                                                                                                                                                                                                                                                                                                            Grimes, Stephen
Karr, Stephen
                                                                                                                                                                                                                                                                                                                                                                            Michaeli, Dov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; ilarity 100.0%; Conservative 0
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   100.0%;
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 Score 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 75; DB 1
Pred. No. 0.04;
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DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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Length 12;
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; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: pyroglutamic acid
US-09-700-378-5
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
PCT-US94-04832A-73
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US-09-700-378-5
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SEQ ID NO 5
LENGTH: 12
TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                      Sequence 73, Application PC/TUS9404832A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity
Matches 12; Conserv
                                                     ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V6
CURRENT APPLICATION DATA:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/700,378
CURRENT FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: PT/US99/10734
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE:
                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                              TITLE OF INVENTION: Immunogenic LHRH peptide constructs TITLE OF INVENTION: and synthetic universal immune stimulators NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                    STATE: N
COUNTRY:
ZIP: 115
              CLASSIFICATION:
                            APPLICATION NUMBER: FILING DATE: 13-AP
                                                                                                                                                                                                 STREET: 400 Garden City
                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ELGPQGRPPPPC 12
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                                                                                                                                                                                                               400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Karr, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stephen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gevas, Philip
                                                                                                                                                                                                                                                                                                           Wang, Chang Yi
Zamb, Timothy
                                                                                                                                                                                                                                                                                                                                         Ladd,
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                              13-APR-1994
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                                                                                                                                                                                                                                                                                                                                         Anna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Method for the Treatment of Gastroesophageal Reflux Disease
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                                         PCT/US94/04832A
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                                                                          Version #1.25
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Best Local Similarity 81.8
"^+^hes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (516)742-4343
TELEPHONE: (516)742-4343
TELEFAX: (516)742-4366
INFORMATION FOR SEQ 1D NO: 73:
                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Immunogenic Peptides Which Contain LHRH
TITLE OF INVENTION: And A Helper T-Cell Epitope For Treatment Of Prostate Cancer
TITLE OF INVENTION: And Induction Of Infertility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: li
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LENGTH: 11 amino acids
                                                                                                                  REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
TELEFAX: (212)751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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 MOLECULE TYPE:
                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                 FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/229,275
FILING DATE: 14-APR-1994
APPLICATION NUMBER: 08/057,166
FILING DATE: 27-APR-1993
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: Ub/w...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: UB/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                   NAME: Maria C. H. L. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07
CLASSIFICATION:
                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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Zamb, Timothy
                                                11 amino acids
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peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                      08/488,351
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                                                                                                                                                                                 29,323
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PCT-US01-14827-14717

Sequence 14717, Application PC/TUS0114827

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc

ITILE OF INVENTION: NOVEL NUCLEIC ACIDS AND POI

FILE REFERENCE: 21272-104

CURRENT APPLICATION NUMBER: PCT/US01/14827

CURRENT FILING DATE: 2001-05-16

PRIOR APPLICATION NUMBER: 09/577,408

PRIOR FILING DATE: 2000-05-18

NUMBER: OF SEQ ID NOS: 16102
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                   Query Match
Best Local Similarity
"---hes 8; Conserva
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: LOCATION: (1)...(160)

: OTHER INFORMATION: Xaa =

PCT-US01-14827-14717
                                                                                                    PCT-US01-08656-6637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US01-08656-6637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 10994
SOFTWARE: CUSTOM
SEQ ID NO 6637
LENGTH: 139
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6637, Application PC/TUS0108656 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 14717
LENGTH: 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 74. Best Local Similarity 81. Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/770,160 PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/522,929 PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: PCT/US01/08656
CURRENT FILING DATE: 2001-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Custom
                                                                                                                  NAME/KEY: misc_feature
LOCATION: (1)...(139)
OTHER INFORMATION: Xaa = X or * as defined in Table 2
                                                                                                                                                                  FEATURE:
                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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1 ELGPQGRPPPP
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81.8%;
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Pred.
                                                 Score 55; DB
Pred. No. 88;
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                                   Mismatches
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6.7;
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                                                                   Length 139;
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                                   Indels
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                                   0,
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QISPQGRPPPP

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Sequence 6639, Application PC/TUS0108656
GENERAL, INFORMATION:
GENERAL STREET, SEC. TO SEC. TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC AC:
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: PCT/US01/08656
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
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Matches 8
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SEQ ID NO 6639
LENGTH: 169
TYPE: PRT
                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 638
SOFFWARE: Patentin Ver. 2.0
SEQ ID NO 470
LENGTH: 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 470, Application US/09758444
GENERAL INFORMATION:
APPLICANT: Rosen et al.
                               NAME/KEY: SITE
LOCATION: (75)
OTHER INFORMATION: )
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/758,444
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PM032
                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo :
FEATURE:
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                                                                                         NAME/KEY: SITE LOCATION: (74) OTHER INFORMATION:
                                                                                                                                    NAME/KEY: SITE LOCATION: (73) OTHER INFORMATION:
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   OTHER INFORMATION:
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                  OCATION:
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                                                    Matches
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Best Local
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LENGTH: 323
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local
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PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/758,444
CURRENT FILING DATE: 2001-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: \mbox{PM}32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
                                                                                                                                                       LOCATION: (293)
OTHER INFORMATION:
                                                                                                                             NAME/KEY: SITE
LOCATION: (319)
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OTHER INFORMATION:
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NAME/KEY: SITE
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LOCATION: (198)
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OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: SITE
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32 GPVGPPPPPC 41
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Pred. No.
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Pred. No. 2.6e
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RESULT 12 US-10-212-160-476

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US-10-015-127-10407; Sequence 10407, Application US/10015127; GENERAL INFORMATION:
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SEQ ID NO 476
LENGTH: 323
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                        APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Sphingomonas elodea genome sequences
FILE REFERENCE: 38-10(15806)B
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NUMBER OF SEQ ID NOS: 638
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PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PM032ClN
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CURRENT FILING DATE:
               CURRENT
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature LOCATION: (319)
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OTHER INFORMATION: Xaa
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             APPLICATION NUMBER:
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2001-10-29
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; ORGANISM: Sphingomonas elodea US-10-015-127-10407
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APPLICANT: ALEXANDROV, NICKO
APPLICANT: CHEN, Xianfeng
APPLICANT: SUBRAMANIAN, Gopa
APPLICANT: ZHENG, Liansheng
TITLE OF INVENTION: SEQUENCE:
FILE REFERENCE: 2750-0662P
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                                                   ; OTHER INFORMATION: any n or Xaa US-09-451-320-4290
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US-09-451-320-4290
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CURRENT FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 3978
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 962, Application PC/TUS9922855 GENERAL INFORMATION: APPLICANT: Ceres, Inc.
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LENGTH: 172
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SOFTWARE: PatentIn Ve
SEQ ID NO 4290
LENGTH: 222
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Best Local
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Best Local Similarity
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PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 14357
                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/451,320 CURRENT FILING DATE: 1999-12-01 NUMBER OF SEQ ID NOS: 6998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding TITLE OF INVENTION: Polypeptides Encoded Thereby FILE REFERENCE: 2750-0567F(PC)
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TYPE: PRT
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OTHER INFORMATION: any n or Xaa FEATURE:
                                                                                                    ORGANISM: Arabidopsis thaliana
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                                                                                     FEATURE:
                                                                                                                        TYPE: PRT
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nes 9; Conserv
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les 8; Conserv
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                                                                                                                                                                                                                                                                                                                                     ALEXANDROV, Nickolai
                                                                                                                                                                                                                                                          ZHENG, Liansheng
VENTION: SEQUENCE-DETERMINED DNA FRAGMENTS 42-59,
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75.0%;
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Pred. No. 2.7e+02;
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Pred. No. 2
 Score 51; DB 18;
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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   score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.
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75
   Pending_Patents_AA_New:*
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/cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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US-09-724-676-88535
US-09-724-676-88539
US-09-724-676A-88523
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724-676-88527
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Compugen Ltd
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ALIGNMENTS	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50
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	Sequence 885	Sequence 88:	Sequence 889	Sequence 889	Sequence 885	Sequence 885	Sequence 8853	Sequence 88521	Sequence 8852	Sequence 889	Sequence 8851	Sequence 88531	Sequence 889	Sequence 88521	Sequence 8852	Sequence 8852:	Sequence 8851	Sequence 88!	Sequence 885
	529,	8524,	88520,	533,	38533,	88538,	531,	528,	526,	522,	518,	538,	531,	528,	526,	522,	518,	88541,	537,
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#### ; NAME/KEY: MOD_RES; LOCATION: (1)..(1); OTHER INFORMATION: pyroglutamic acid US-10-314-057-5 RESULT 2 US-10-154-678-58 RESULT 1 US-10-314-057-5 B δÃ Sequence 58, Application US/10154678 GENERAL INFORMATION: APPLICANT: Benjanin, Stephane APPLICANT: Tanaka, Hiroaki TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF FILE REFERENCE: 182.US1.REG CUGRENT APPLICATION UNMER: US/10/154,678 CURRENT FILING DATE: 2002-10-15 Query Match Best Local S SEQ ID NO 5 LENGTH: 12 Sequence 5, Application US/10314057 GENERAL INFORMATION: Matches APPLICANT: Gevas, Philip APPLICANT: Stephen, Grimes APPLICANT: Stephen, Grimes APPLICANT: Wichaeli, Dov TITLE OF INVENTION: Method for the Treatment of Gastroesophageal Reflux Disease FILE REFERENCE: ACGIUSA CURRENT APPLICATION NUMBER: US/10/314,057 CURRENT FILING DATE: 2002-12-06 PRIOR APPLICATION NUMBER: US/09/700,378 PRIOR APPLICATION NUMBER: US/09/10734 PRIOR APPLICATION NUMBER: DS/05-14 PRIOR APPLICATION NUMBER: 60/085,610 PRIOR FILING DATE: 1999-05-14 PRIOR APPLICATION NUMBER: 60/085,610 PRIOR FILING DATE: 1998-05-15 NUMBER OF THE NOTE: 1998-05-15 NUMBER OF THE NOTE: 1998-05-15 NUMBER OF SEQ ID NOS: 8 SOFTWARE: PatentIn version TYPE: PRT ORGANISM: human FEATURE: Local Similarity nes 12; Conserv 1 ELGPQGRPPPPC 12 ||||||||||| 1 ELGPQGRPPPPC 12 Conservative 100.0%; 0; Score 75; Pred. No. Mismatches 0 DB 6; .0038; Length 12; Indels 0 Gaps 0;

Sequence Sequence Sequence

Sequence

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PRIOR FILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: US 09/924,340

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US-09-724-676A-88534

Sequence 88534, Application US/09724676A

GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEO ID NO 88534

LENCTH: 265
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 88534
LENGTH: 265
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676-88534
                                                                  ; ORGANISM: Homo sapiens US-09-724-676A-88534
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US-09-724-676-88534
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PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2011-05-25
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LENGTH: 163
                                 Query Match
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Best Local :
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Pred. No.
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            Score 50; DB
Pred. No. 43;
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Mismatches
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RESULT 7
US-09-724-676-88527
Sequence 88527, Application US/09724676
; GENERAL INFORMATION:
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Best Local Similarity
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US-09-724-676-88523
US-09-724-676-88523, Application US/09724676
GENERAL INFORMATION:
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US-09-724-676-88519
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER of SEO ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 88523
LENGTH: 319
TYPE: PRT
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SEQ ID NO 88519
LENCTH: 319
TYPE: PRT
                    SOFTWARE: PatentIn version 3.2
SEQ ID NO 88527
LENGTH: 319
TYPE: PRT
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                                                                                  FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
                                                                                                                                                           APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing
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ORGANISM: Homo sapiens
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US-09-724-676-88532
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 88535
LENGTH: 319
                                                                                        Sequence 88539, Application US/09724676 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 88532
LENGTH: 319
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         APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION NUMBER: US/09/724,676 CURRENT FILING DATE: 2000-11-28
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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RESULT 13
US-09-724-676A-88527
Sequence 88527, Application US/09724676A
; GENERAL INFORMATION:
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US-09-724-676A-88523
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US-09-724-676A-88519
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 88523
LENGTH: 319
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 88519
LENGTH: 319
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SEQ ID NO 88539
LENGTH: 319
TYPE: PRT
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TYPE: PRT
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APPLICANT: Compugen LTD

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RESULT 15
US-09-724-676A-88535
US-09-724-676A-88535
Sequence 88535, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILLING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 88535
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676A-88535
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 88532
LENGTH: 319
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; ORGANISM: Homo sapiens
US-09-724-676A-88527
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US-09-724-676A-88532
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Matches 8
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                                                            Query Match 66.7
Best Local Similarity 88.9
Matches 8; Conservative
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Search completed: February 5, 2003, 09:50:58 Job time: 19.4286 secs